

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 70.555 Seconds
(without alignments)
2650.131 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	5882	99.3	1178	21	AAAY71311	Human neurite grow	
2	5815	98.2	1192	22	AAU04591	Human Nogo protein	
3	5815	98.2	1192	23	ABP68600	Human pancreatic c	
4	5810	98.1	1192	21	AAAY56967	Human MAGI polypep	
5	5810	98.1	1192	22	AAB82349	Human NOGO-A prote	
6	5810	98.1	1192	23	ABB81078	Human neurotransmi	
7	5810	98.1	1192	23	ABG30938	Human NogoA protei	
8	5526.5	93.3	1246	22	AAU33228	Novel human secret	
9	4560	77.0	983	24	ABU11573	Human MDDT polypep	
10	4400	74.3	893	21	AAAY95012	Human secreted pro	
11	4296.5	72.5	1163	21	AAAY71310	Rat neurite growth	
12	4296.5	72.5	1163	23	ABB81074	Rat neurotransmitt	
13	4294.5	72.5	1162	21	AAAY71557	Rat Nogo A truncat	
14	4286.5	72.4	1163	21	AAAY71384	Alternative versio	
15	3388.5	57.2	974	21	AAAY71560	Rat Nogo A protein	
16	3146.5	53.1	642	19	AAW58383	Human secreted pro	
17	3146.5	53.1	642	22	AAB90682	Human BG160_1 prot	
18	2715	45.8	803	21	AAAY71562	Rat Nogo A protein	
19	2529.5	42.7	737	21	AAAY71386	Rat Nogo A protein	
20	2487.5	42.0	746	21	AAAY71391	Rat Nogo A protein	
21	2457	41.5	736	21	AAAY71398	Rat Nogo A protein	
22	2449.5	41.4	732	21	AAAY71399	Rat Nogo A protein	
23	2405.5	40.6	695	21	AAAY71387	Rat Nogo A protein	
24	2344.5	39.6	684	21	AAAY71394	Rat Nogo A protein	
25	1948.5	32.9	552	21	AAAY71388	Rat Nogo A protein	
26	1743	29.4	502	21	AAAY71396	Rat Nogo A protein	
27	1634.5	27.6	475	21	AAAY71389	Rat Nogo A protein	
28	1566.5	26.4	403	21	AAAY71563	Rat Nogo A protein	
29	1552.5	26.2	457	21	AAAY71392	Rat Nogo A protein	
30	1495.5	25.2	373	21	AAB24242	Human Nogo B prote	
31	1495.5	25.2	373	21	AAAY56969	Human MAGI polypep	
32	1495.5	25.2	373	21	AAAY53624	A bone marrow secr	
33	1495.5	25.2	373	22	AAB82350	Human NOGO-B prote	
34	1495.5	25.2	373	23	ABP68601	Human pancreatic c	
35	1495.5	25.2	373	23	ABB81079	Human neurotransmi	
36	1495.5	25.2	373	23	AAM47954	Human RTN4B SEQ ID	
37	1487.5	25.1	373	23	ABG30937	Human NogoB protei	
38	1412	23.8	289	21	AAAY56968	Human MAGI polypep	
39	1327	22.4	284	21	AAAY95030	Human clone vb22_1	
40	1264	21.3	356	21	AAAY71390	Rat Nogo A protein	
41	1205.5	20.4	374	21	AAAY71397	Rat Nogo A protein	
42	1196.5	20.2	361	21	AAAY71385	Alternative versio	
43	1189	20.1	359	21	AAAY71558	Rat Nogo A protein	
44	1187	20.0	360	21	AAAY71383	Rat neurite growth	
45	1187	20.0	360	23	ABB81076	Rat neurotransmitt	

ALIGNMENTS

RESULT 1

AAY71311

ID AAY71311 standard; Protein; 1178 AA.

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AC AAY71311;

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DT 02-NOV-2000 (first entry)

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DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 187

FT /label= Unknown

FT Misc-difference 188

FT /label= Unknown

FT Misc-difference 189

FT /label= Unknown

FT Misc-difference 190

FT /label= Unknown

FT Misc-difference 221

FT /label= Unknown

FT Misc-difference 328

FT /label= Unknown

FT Misc-difference 477

FT /label= Unknown

FT Region 994..1174

FT /note= "Region specifically described in claim 16"

FT Region 977..1012

FT /note= "Region specifically described in claim 16"

FT Region 1079..1114

FT /note= "Region specifically described in claim 16"

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PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX

PS Claim 11; Fig 13; 122pp; English.

XX

CC The present sequence is a human Nogo protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC human Nogo sequence was derived by aligning human expressed sequence tags
CC (ESTs) e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565,
CC AA081525 and AA081840 with the rat Nogo sequence.
CC Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC meningioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 1178 AA;

Query Match 99.3%; Score 5882; DB 21; Length 1178;
Best Local Similarity 99.7%; Pred. No. 1.8e-297;
Matches 1175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSVPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
QY	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
QY	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
QY	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN	240
Db	181	SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN	240
QY	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300
Db	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300

Qy	301	IVANPREEII VKNKDEEEKLVSNNILHXQQELPTALT KL VKED EVVSSEKAKDSFNEKRV	360
Db	301	IVANPREEII VKNKDEEEKLVSNNILHXQQELPTALT KL VKED EVVSSEKAKDSFNEKRV	360
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH	420
Db	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH	420
Qy	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDE	480
Db	421	EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDE	480
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT KV TEEVVANMPEGLTPDL	540
Db	481	KKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT KV TEEVVANMPEGLTPDL	540
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Qy	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Qy	721	EDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI EYENKEKLSALPPEG	780
Db	721	EDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI EYENKEKLSALPPEG	780
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDL FISKEAQIRE	840
Db	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDL FISKEAQIRE	840
Qy	841	TETFSDDSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	841	TETFSDDSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE	960
Db	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE	960
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDI KKTGVVFGASLFLLLSLTVF	1020
Db	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDI KKTGVVFGASLFLLLSLTVF	1020
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

Db 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

RESULT 2

AAU04591

ID AAU04591 standard; Protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;

KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;

KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;

KW Canavan's disease; metachromatic leukodystrophy; viral infection;

KW Krabbe's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1054..1119

FT /label= Lumenal_extracellular_domain

FT /note= "This sequence is specifically claimed"

FT Peptide 1055..1094 ✓

FT /label= Pep1

FT /note= "Receptor binding inhibitory peptide. This

FT sequence is specifically claimed"

FT Peptide 1064..1088

FT /label= Pep2

FT /note= "Receptor binding inhibitory peptide. This

FT sequence is specifically claimed"

FT Peptide 1074..1098

FT /label= Pep3

FT /note= "Receptor binding inhibitory peptide. This

FT sequence is specifically claimed"

FT Peptide 1084..1108

FT /label= Pep4

FT /note= "Receptor binding inhibitory peptide. This

FT sequence is specifically cly

-- 18550X-

FT Peptide 1095..1119

FT /label= Pep5

FT /note= "Receptor binding inhibitory peptide. This

FT sequence is specifically claimed"

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PN WO200151520-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US01041.

XX

PR 12-JAN-2000; 2000US-0175707.

PR 26-MAY-2000; 2000US-0207366.
PR 29-SEP-2000; 2000US-0236378.

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PA (UYYA) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2001-442138/47.

DR N-PSDB; AAS09453.

XX

PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders -

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PS Example 1; Page 101-104; 109pp; English.

XX

CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon
CC growth inhibitor. The invention relates to the use of the nogo receptor,
CC nogo protein, their nucleic acids, vectors expressing them and antibodies
CC against them, to isolate agents which block nogo receptor mediated axonal
CC growth. The agent is useful for treating a central nervous system
CC disorder which is a result of cranial or cerebral trauma, spinal cord
CC injury, stroke or a demyelinating disease selected from multiple
CC sclerosis, monophasic demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC Spongy degeneration, Alexander's disease, Canavan's disease,
CC metachromatic leukodystrophy, viral infection and Krabbe's disease.

XX

SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 22; Length 1192;
Best Local Similarity 97.2%; Pred. No. 5.6e-294;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLKPKA 60
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Db      1 MEDLDQSPMVSXSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVL  A 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
          |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
          |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
          |||:
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
          |||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
          |||
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Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNNQELPTALTCLKVKEDEVV 360
 Qy 347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 Qy 407 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480
 Qy 467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
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 Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540
 Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGKIAIYETKMDLVQTSEVMQESLYPAAQLCPSF 586
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 Db 541 EVVANMPEGLTPDLVQEACESELNEVTGKIAIYETKMDLVQTSEVMQESLYPAAQLCPSF 600
 Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
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 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPPDFSDYSE 705
 ||||||| ||||||||||||||||||||||||||||||||||||||||||||
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPPDFSDYSE 720
 Qy 706 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 765
 ||||||| ||||||||||||||||||||||||||||||||||||||||||||
 Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 780
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTA
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 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
 Qy 826 SNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 885
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 Db 841 SNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 900
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGH 945
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 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALA- 959
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGV 1005
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 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVT SFRIYKGVIAIQKSDEGHPFRAYLES 1065
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 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1125
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 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 3

ABP68600

ID ABP68600 standard; Protein; 1192 AA.

XX

AC ABP68600;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour.

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OS Homo sapiens.

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PN WO200260317-A2.

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PD 08-AUG-2002.

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PF 30-JAN-2002; 2002WO-US02781.

XX

PR 30-JAN-2001; 2001US-265305P.

PR 31-JAN-2001; 2001US-265682P.

PR 09-FEB-2001; 2001US-267568P.

PR 21-MAR-2001; 2001US-278651P.

PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.

PR 12-JUL-2001; 2001US-305484P.

PR 20-AUG-2001; 2001US-313999P.

PR 27-NOV-2001; 2001US-333626P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;

XX

DR WPI; 2002-627435/67.

DR N-PSDB; ABV94680.

XX

PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
PT for diagnosing, preventing and/or treating cancer, particularly
PT pancreatic cancer -

XX

PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC (b) complements of (a); (c) sequences consisting of at least 20
CC contiguous residues of (a); (d) sequences that hybridize to (a), under
CC moderately stringent conditions; (e) sequences having at least 75% or 90%
CC identity to (a); or (f) degenerate variants of (a). Polypeptides
CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
CC detect cancer in a patient and compositions comprising polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations and
CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The

CC polynucleotides can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 23; Length 1192;
Best Local Similarity 97.2%; Pred. No. 5.6e-294;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

```
Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      |||
Db    241 LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
      |||
Db    301 GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      |||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480

Qy    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
      |||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTGIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      |||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTGIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600

Qy    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
      |||
Db    601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660
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PD 03-FEB-2000 .
XX
PF 21-JUL-1999; 99WO-GB02360 .
XX
PR 22-JUL-1998; 98GB-0016024 .
PR 19-JUL-1999; 99GB-0016898 .
XX
PA (SMIK) SMITHKLINE BEECHAM PLC .
XX
PI Michalovich D, Prinjha RK;
XX
DR WPI; 2000-182693/16 .
DR N-PSDB; AAZ56886 .

Query Match 98.1%; Score 5810; DB 21; Length 1192;
Best Local Similarity 97.2%; Pred. No. 1e-293;
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDELEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDELEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNIILHXQQELPTALTCLKVKEDEVV	346

Db	301		GSSFSVSPKAESAVIVANPREEI	IVKNKDEEEKLVSNNILHNQQELPTALT	TKLVKEDEVV	360	
Qy	347		SSEKAKDSFNEKRVAVEAPMREEYADFKP	FERVWEVKDSKEDSDMLAAGGKIESNLESKV		406	
Db	361		SSEKAKDSFNEKRVAVEAPMREEYADFKP	FERVWEVKDSKEDSDMLAAGGKIESNLESKV		420	
Qy	407		DKKCFADSLEQTNHEKDSSESNDDTSFP	STPEGIKDRSGAYITCAPFNPAATESIATNIF		466	
Db	421		DKKCFADSLEQTNHEKDSSESNDDTSFP	STPEGIKDRPGAYITCAPFNPAATESIATNIF		480	
Qy	467		PLLEDPTSENXTDEKKIEEKKAQIVTEK	NTSTKTSNPFFVAAQDSETDYVTTDNLT	TKVTE	526	
Db	481		PLLGDPPTSENKTDEKKIEEKKAQIVTEK	NTSTKTSNPFLVAAQDSETDYVTTDNLT	TKVTE	540	
Qy	527		EVVANMP	TPDLVQEACESELNEVTGTKIAYETKMD	LVQTSEVMQESLYPAAQLCPSF	586	
Db	541		EVVANMPEGLTPDLVQEACESELNEVTG	TKIAYETKMDLVQTSEVMQESLYPAAQLCPSF		600	
Qy	587		EESEATPSPVLPDI	VMEAPLNSAVPSAGASVIQSSSPLEASSV	NYESIKHEPENPPPYE	646	
Db	601		EESEATPSPVLPDI	VMEAPLNSAVPSAGASVIQSSSPLEASSV	NYESIKHEPENPPPYE	660	
Qy	647		EAMSVSL-KVSGIKEEIKEPENINAALQ	ETEAPYISIIACDLIKETKLSAEPAPDF	SDYSE	705	
Db	661		EAMSVSLKKVSGIKEEIKEPENINAALQ	ETEAPYISIIACDLIKETKLSAEPAPDF	SDYSE	720	
Qy	706		MAKVEQPVPDHSELVEDSSPDSEPVDL	FSDDSI	PDVPQKQDETVM	LVKESLTETSFESMI 765	
Db	721		MAKVEQPVPDHSELVEDSSPDSEPVDL	FSDDSI	PDVPQKQDETVM	LVKESLTETSFESMI 780	
Qy	766		EYENKEKLSALPPEGGKPYLESFKLSLD	NTKDTLLPDEVSTLSKKEKI	PLQMEELSTAVY	825	
Db	781		EYENKEKLSALPPEGGKPYLESFKLSLD	NTKDTLLPDEVSTLSKKEKI	PLQMEELSTAVY	840	
Qy	826		SNDDLFI	SKEAQIRETETFS	DSSPIEII	IDEFPTLISSKTD	SFSKLAREYTDLEVSHKSEI 885
Db	841		SNDDLFI	SKEAQIRETETFS	DSSPIEII	IDEFPTLISSKTD	SFSKLAREYTDLEVSHKSEI 900
Qy	886		ANAPDGAGSLPCTELPHDLSLKNIQPK	VEEKISFSDDFS	SKNGSATS	SKVLLLPPDVS	ALGH 945
Db	901		ANAPDGAGSLPCTELPHDLSLKNIQPK	VEEKISFSDDFS	SKNGSATS	SKVLLLPPDVS	SALA- 959
Qy	946		TQAEIESIVKPKVLEKEAEKKLP	SDTEKEDRSPSAIFSADLGKTS	SVVDLLYWRDI	KKTGV 1005	
Db	960		TQAEIESIVKPKVLVKEAEKKLP	SDTEKEDRSPSAIFS	AE	SVVDLLYWRDI	KKTGV 1019
Qy	1006		VFGASLFL	LLSLTVFSIVSVTAYIALALLSVTIS	FRIIYKGVIAIQKS	DEGHPFRAYLES 1065	
Db	1020		VFGASLFL	LLSLTVFSIVSVTAYIALALLSVTIS	FRIIYKGVIAIQKS	DEGHPFRAYLES 1079	
Qy	1066		EVAISEELVQKYSNSALGHVNCTI	KELRRLFLVDDL	VDSLKFAVLMWVFTY	VGALFNGLT 1125	
Db	1080		EVAISEELVQKYSNSALGHVNCTI	KELRRLFLVDDL	VDSLKFAVLMWVFTY	VGALFNGLT 1139	
Qy	1126		LLILALISLFSVPVIYERHQAQIDHYL	GLANKNVKDAMAKIQAKI	PGLKRKAE	1178	

Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLI SSKTDSFSK LAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLI SSKTDSFSK LAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI SFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI SFSDDFSKNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAI FSADLGKTSVVDLL YWRDI KKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLP SDTEKEDRSPSAI FSAELSKTSVVDLL YWRDI KKTGV	1019
Qy	1006	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIQAI QKSDEGHPFRAYLES	1065
Db	1020	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIQAI QKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTI KELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTI KELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI PGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI PGLKRKAE	1192

RESULT 6

ABB81078

ID ABB81078 standard; Protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-0893348.

XX

PR 19-MAY-1998; 98IL-0124500.
PR 21-JUL-1998; 98WO-US14715.
PR 22-DEC-1998; 98US-0218277.
PR 19-MAY-1999; 99US-0314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86601.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -

XX

PS Examples; Page 53-56; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the human
CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
CC antigen.

XX

SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 23; Length 1192;

Best Local Similarity 97.2%; Pred. No. 1e-293;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

QY 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Db	1	MEDLDQSPLVSSSDSPRRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEII VKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEII VKNKDEEEKLVSNNILHNNQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKKEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKKEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885

Db 841 SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 900
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LLLPPDV SALGH 945
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LLLPPDV SALA- 959
 Qy 946 TQAEIESIVKPKVLEKEAEKKLP S DTEKEDRSPSAIF S ADLGKTSVVDLLYWRDIKKTGV 1005
 |||||||||||||| |||||||||||||||||||||||||:| ||||||||||||||||
 Db 960 TQAEIESIVKPKVLVKEAEKKLP S DTEKEDRSPSAIF S AELSKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASL FLLL SLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFRAYLES 1065
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1020 VFGASL FLLL SLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1125
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1192

RESULT 7

ABG30938

ID ABG30938 standard; Protein; 1192 AA.

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AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis.

XX

OS Homo sapiens.

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB00228.

XX

PR 18-JAN-2001; 2001GB-0001312.

XX

PA (GLAX) GLAXO GROUP LTD.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR N-PSDB; ABK90134.

Qy 287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
 |||
 Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNNQQELPTALTCLKVKEDEVV 360
 |||
 Qy 347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
 |||
 Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420
 |||
 Qy 407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
 |||
 Db 421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480
 |||
 Qy 467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
 |||
 Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540
 |||
 Qy 527 EVVANMPEGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
 |||
 Db 541 EVVANMPEGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
 |||
 Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
 |||
 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660
 |||
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 705
 |||
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE 720
 |||
 Qy 706 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 765
 |||
 Db 721 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 780
 |||
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
 |||
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
 |||
 Qy 826 SNDDLFIKSEAQIRETETFSDDSPIEII DEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 885
 |||
 Db 841 SNDDLFIKSEAQIRETETFSDDSPIEII DEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 900
 |||
 Qy 886 ANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFS KN GSATSKVLLLPPDV SALGH 945
 |||
 Db 901 ANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFS KN GSATSKVLLLPPDV SALA- 959
 |||
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV 1005
 |||
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
 |||
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 |||
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 |||
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
 |||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
 |||
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 1140 |||L|L|A|L|I|S|L|F|S|V|P|V|I|Y|E|R|H|Q|A|I|D|H|Y|L|G|L|A|N|K|N|V|K|D|A|MA|K|I|Q|A|K|I|P|G|L|K|R|K|A|E 1192

RESULT 8

AAU33228

ID AAU33228 standard; Protein; 1246 AA.

XX

AC AAU33228;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3719.

XX

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US08656.

XX

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -

XX

PS Claim 20; Page 737; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

XX

SQ Sequence 1246 AA;

Query Match 93.3%; Score 5526.5; DB 22; Length 1246;
Best Local Similarity 93.0%; Pred. No. 5.9e-279;
Matches 1123; Conservative 13; Mismatches 39; Indels 33; Gaps 10;

```
Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db     42 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 101

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
      |||
Db    102 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 161

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    162 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 221

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:      :      : |||
Db    222 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 281

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      |||
Db    282 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 341

Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEV 346
      |||
Db    342 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEV 401

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    402 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 461

Qy    407 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 466
      |||
Db    462 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 521

Qy    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTE 526
      |||
Db    522 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLLVAAQDSETDYVTTDNLTKVTE 581

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      |||
Db    582 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 641

Qy    587 EESEATPSPVLPDI VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESI KHEPENPPPPYE 646
      |||
Db    642 EESEATPSPVLPDI VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESI KHEPENPPPPYE 701

Qy    647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705
      |||
Db    702 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 761

Qy    706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI 765
      |||
```

Db 762 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI 821

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY 825
 |||

Db 822 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY 881

Qy 826 SNDDLFISKEAQIRETETFS DSSPIEI IDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 |||

Db 882 SNDDLFISKEAQIRETETFS DSSPIEI IDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 941

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGH 945
 |||

Db 942 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALA- 1000

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV 1005
 |||

Db 1001 TQAEIESIVKPKVLVKEAEKKLPSTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1060

Qy 1006 VFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAY-- 1062
 ||| : |||

Db 1061 VFGASAVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAISG 1120

Qy 1063 -LESEVAISEELVQKYSNSALGHV-NCTIKELRR--LFLVDDLVD SLK-FAVLMWVFTY 1116
 || : : | : ||| : ||| : | | ||| : |||

Db 1121 NLESCLYLRELGSGRYSNSALGSMWNCTVKGNFRAPSF FSWMDLVDSLRSFAVLMWVFTY 1180

Qy 1117 VGALFNGLTLL-----ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1170
 || | || : | || : ||| : |||

Db 1181 VGCL--GLMVLDTTGFWALNFISSSGSWLIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1238

Qy 1171 PGLKRKAE 1178
 |||

Db 1239 PGLKRKAE 1246

RESULT 9

ABU11573

ID ABU11573 standard; Protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US09944.
 XX
 PR 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.
 PR 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-058431/05.
 DR N-PSDB; ABX34563.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis -
 XX
 PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 983 AA;

Query Match 77.0%; Score 4560; DB 24; Length 983;
 Best Local Similarity 97.1%; Pred. No. 7.8e-229;
 Matches 919; Conservative 8; Mismatches 11; Indels 8; Gaps 3;

Qy	240	NLSTVL-----PTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVS	293
Db	39	NMNTLVICQYYPLKEHFKNVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVS	98
Qy	294	PKAESAVIVANPREEII VKNKDEEEKLVSNNILHXQQELPTALTCLKVEDEVVSSEKAKD	353
Db	99	PKAESAVIVANPREEII VKNKDEEEKLVSNNILHNQQELPTALTCLKVEDEVVSSEKAKD	158
Qy	354	SFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFAD	413
Db	159	SFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFAD	218
Qy	414	SLEQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPT	473
Db	219	SLEQTNHEKDSSESSNDTSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDP	278
Qy	474	SENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMP	533
Db	279	SENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMP	338
Qy	534	EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATP	593
Db	339	EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATP	398
Qy	594	SPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESI KHEPENPPPYEEAMSVSL	653
Db	399	SPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESI KHEPENPPPYEEAMSVSL	458
Qy	654	-KVSGIKKEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP	712
Db	459	KKVSGIKKEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP	518
Qy	713	VPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI EYENKEK	772
Db	519	VPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI EYENKEK	578
Qy	773	LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDLFI	832
Db	579	LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDLFI	638
Qy	833	SKEAQIRETETFSDDSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA	892
Db	639	SKEAQIRETETFSDDSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA	698
Qy	893	GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS KVLVLLPPDV SALGHTQAEIES	952
Db	699	GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS KVLVLLPPDV SALA-TQAEIES	757
Qy	953	IVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDI KKTGVVFGASLF	1012
Db	758	IVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSALSKTSVVDLLYWRDI KKTGVVFGASLF	817
Qy	1013	LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE	1072
Db	818	LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE	877
Qy	1073	LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLIILI	1132

Db 878 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALI 937

Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 938 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 983

RESULT 10

AA95012

ID AAY95012 standard; Protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US19351.

XX

PR 24-AUG-1998; 98US-0097638.

PR 24-AUG-1998; 98US-0097659.

PR 09-SEP-1998; 98US-0099618.

PR 28-SEP-1998; 98US-0102092.

PR 25-NOV-1998; 98US-0109978.

PR 23-DEC-1998; 98US-0113645.

PR 23-DEC-1998; 98US-0113646.

PR 23-AUG-1999; 99US-0379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding
 PT them, useful for treating neurodegenerative disorders, autoimmune
 PT diseases and cancer -

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PS Claim 73; Page 322-325; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
 CC proteins of the invention include those that are thought to be only
 CC partially secreted, i.e., transmembrane proteins. The proteins of the
 CC invention may exhibit one or more activities selected from the following:

CC cytokine activity; cell proliferation; differentiation; immune
 CC modulation; haematopoiesis regulation; tissue growth activity;
 CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
 CC and thrombolytic activity; anti-inflammatory activity; and tumour
 CC inhibition activity. The proteins may be administered to patients as
 CC vaccines, and the nucleotides may be used as part of a gene therapy
 CC regime. Diseases or conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections, especially HIV; multiple sclerosis;
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
 CC insulin dependent diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. The present sequence represents one of the
 CC 40 proteins of the invention.

XX

SQ Sequence 893 AA;

Query Match 74.3%; Score 4400; DB 21; Length 893;
 Best Local Similarity 98.9%; Pred. No. 1.4e-220;
 Matches 884; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

QY	286	MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEV	345
Db	1	MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEV	60
QY	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	405
Db	61	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESK	120
QY	406	VDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	465
Db	121	VDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNI	180
QY	466	FPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVT	525
Db	181	FPLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVT	240
QY	526	EEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	585
Db	241	EEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPS	300
QY	586	FESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY	645
Db	301	FESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY	360
QY	646	EEAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYS	704
Db	361	EEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYS	420
QY	705	EMAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESM	764

Db	421	EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESM	480
Qy	765	IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV	824
Db	481	IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV	540
Qy	825	YSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSE	884
Db	541	YSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSE	600
Qy	885	IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSA LG	944
Db	601	IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSA LA	660
Qy	945	HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTG	1004
Db	661	-TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTG	719
Qy	1005	VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLE	1064
Db	720	VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLE	779
Qy	1065	SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL	1124
Db	780	SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL	839
Qy	1125	TLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	840	TLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	893

RESULT 11

AAY71310

ID AAY71310 standard; Protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 1..171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT Region 31..58

FT		/note= "Acidic region"
FT	Region	31..57
FT		/note= "Region specifically described in claim 16"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242..244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468..470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694..696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912..914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925..927
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	954
FT		/note= "PKC and casein kinase II sites"
FT	Modified-site	956
FT		/note= "PKC and casein kinase II sites"
FT	Domain	988..1023
FT		/label= Transmembrane_domain
FT		/note= "C-terminal hydrophobic region
FT		specifically described in claim 16"

FT Modified-site 1024
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1071..1073
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1073
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
 FT Domain 1090..1125
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region
 specifically described in claim 16"
 FT Modified-site 1141..1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 FT Peptide 623..640
 FT /note= "used as immunogen to generate antibody AS 472"
 FT Peptide 762..1163
 FT /note= "used as immunogen to generate antibody AS Bruna"
 FT Inhibitory-site 542..722
 FT Region 172..259
 FT /note= "This region is not essential for inhibitory
 activity"
 FT Region 975..1162
 FT /note= "This region is not essential for inhibitory
 activity"
 FT Region 976..1163
 FT /note= "C-terminal common region found in Nogo A, B and
 C isoforms"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US26160.
 XX
 PR 06-NOV-1998; 98US-0107446.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 DR N-PSDB; AAD01173.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -
 XX
 PS Claim 3; Fig 2A; 122pp; English.
 XX
 CC The present sequence is a rat Nogo A protein which is a
 CC potent neural cell growth inhibitor and is free of all central nervous
 CC system (CNS) myelin material with which it is natively associated. The
 CC protein was derived from a cDNA generated by fusing R018U37-3, R1-3U21

CC cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord
 CC library, and Olil8 cDNA from an oligo d(T)-primed rat oligodendrocyte
 CC library. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired.
 CC The animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which
 CC can treat or prevent disorders or diseases of the CNS.
 CC Note: The present sequence designated as SEQ ID NO: 2 is stated to
 CC be the same as the sequence shown in Fig. 13 (see AAY71384) of the
 CC specification. However, this sequence does not match the sequence given
 CC in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and
 CC SEQ ID NO: 29 in disclosure of the specification. However, the
 CC specification does not include sequences for these SEQ ID numbers.

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 21; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 4.8e-215;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDDEE-EEEEEEEEDEDEDLEELEVLERK	58
Db	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEDEEEEEDEDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL	224
Db	167	RGSGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Qy	225	SPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLTEFSELEYS	284
Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIETLNEASKELPERATNPVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVAVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396

Qy 404 SKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463
 |||:| | | | : | | | :| | | | | :| | | | | :| | |
 Db 397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455

Qy 464 NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTK 523
 | | | | | | | | | | | | | | :| | | :| | | | | | | | | | | | | | :|
 Db 456 NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514

Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
 ||| :| | | | | | | | | | | | | | | | | | | | | | | | :| | | | | | | |
 Db 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESI KHEPENP 642
 ||| | :| | | | | | | | | | | | | | | | | | | | | | | | | | :| | | | | | | |
 Db 575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPL EAPPPVSYDSI KLEPENP 634

Qy 643 PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702
 ||| | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | :| | | | :
 Db 635 PPYEEAMNVALKALGTKEGKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSN 694

Qy 703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFE 762
 ||| :| | | :| | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E 753

Qy 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822
 :: :: :| :| | | | | | | | | | | :| :| | | :: :| :| | | | | | | :|
 Db 754 TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT 811

Qy 823 AVYSNDDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK 882
 | :| | | | | | | | :| :| :| | | | | | | | | | | | | | | | | | | | | | |
 Db 812 AIYSNDDLLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK 870

Qy 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVS 942
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 871 SEIANIQSGADSLPCLLELPDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA 928

Qy 943 LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002
 | | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 929 L-EPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK 987

Qy 1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1062
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
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 Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 12
 ABB81074
 ID ABB81074 standard; Protein; 1163 AA.

XX
 AC ABB81074;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Rat neurotransmitter receptor protein Nogo-A.
 XX
 KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; receptor.
 XX
 OS Rattus norvegicus.
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-0893348.
 XX
 PR 19-MAY-1998; 98IL-0124500.
 PR 21-JUL-1998; 98WO-US14715.
 PR 22-DEC-1998; 98US-0218277.
 PR 19-MAY-1999; 99US-0314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86600.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides -
 XX
 PS Example 5; Page 44-47; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and

CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the rat
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen.

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 23; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 4.8e-215;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
		:	
Db	1	MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSSL	224
		:	
Db	167	RGSGSVDETFLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Qy	225	SPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS	284
		: : : : :	
Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQLPTALTCLVKEDE	344
		: : : : :	
Db	287	EMGSSFKGSPKGESAILVENTKEEIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
		: : : : :	
Db	341	VVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
		: : : :	
Db	397	SKVDRKCLEDSEKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTK	523
		: : : : :	
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK	514

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX

PS Example; Page -; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is a truncated form of rat Nogo A protein shown
CC in AAY71310, which is used in the construction of mutant Nogo-A. Nogo-A
CC is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-1162.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.
CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the

CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.

XX

SQ Sequence 1162 AA;

Query Match 72.5%; Score 4294.5; DB 21; Length 1162;
Best Local Similarity 74.1%; Pred. No. 6.1e-215;
Matches 885; Conservative 103; Mismatches 156; Indels 51; Gaps 19;

```
Qy      1 MEDLDQSPLVSSS-DSPPRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEDIDQSSLVSSSTDSPPRPPAPFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60

Qy     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 PAAGLSAAAVP--PAAAAPLLDfSSDSVFPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKR 178
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy    179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    167 RGSGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy    225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    227 SPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy    285 EMGSSFSVSPKAESAVIVANPREEI IVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE 344
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy    345 VVSSEKAKDSFNEKRAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    341 VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE 396

Qy    404 SKVDKKCFADSLEQTNHEKDSSESSNDTSTFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455

Qy    464 NIFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLT 523
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    456 NTFPILLEDHTSENKTDEKKIEERKAQII TEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514

Qy    524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy    584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP 642
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENP 634

Qy    643 PPYEEAMSVSLKVSIGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD 702
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    635 PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSDFSN 694
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FT		/note= "Casein kinase II site"
FT	Region	31..58
FT		/note= "Acidic region"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242..244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468..470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694..696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
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FT	Modified-site	868
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FT	Domain	988..1023
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FT		/note= "C-terminal hydrophobic region"
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FT /note= "Asn is N-glycosylated"
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 FT /note= "used as immunogen to generate antibody AS 472"
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 FT Inhibitory-site 542..722
 FT Region 172..259
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 975..1162
 FT /note= "This region is not essential for inhibitory
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 FT Region 976..1163
 FT /note= "C-terminal common region found in Nogo A, B and
 FT C isoforms"
 FT Misc-difference 223
 FT /label= Unknown
 FT /note= "There is Leu at this position in the
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 FT Misc-difference 404
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 FT Misc-difference 469
 FT /label= Unknown
 FT /note= "There is Lys at this position in the
 FT sequence shown in AAY71310"
 FT Misc-difference 661
 FT /note= "There is Asn at this position in the
 FT sequence shown in AAY71310"
 FT Misc-difference 820
 FT /note= "There is Leu at this position in the
 FT sequence shown in AAY71310"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US26160.
 XX
 PR 06-NOV-1998; 98US-0107446.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX

PS Claim 3; Fig 13; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all
CC central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying
CC neurite growth inhibitory activity are used in the
CC treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: The present sequence is an alternative version of the
CC Nogo A sequence shown in Fig. 2A (see AAY71310).
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 1163 AA;

Query Match 72.4%; Score 4286.5; DB 21; Length 1163;
Best Local Similarity 74.1%; Pred. No. 1.6e-214;
Matches 886; Conservative 104; Mismatches 155; Indels 51; Gaps 19;

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      ||||| ||| ||| |||: ||| : ||||| ||||| ||||| ||||| : || : |
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Qy    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
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Qy    179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
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Qy    225 SPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
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Db	287	EMGSSFKGSPKGESAILVENTKKEEIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
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Qy	464	NIFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTK	523
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Qy	584	PSFEESEATPSPVLPDI VMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP	642
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Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSI PEVPQTQEEAVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISIQMEEFNT	811
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Db	929	L-EPQTEMGSI VKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
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RESULT 15

AA71560

ID AAY71560 standard; Protein; 974 AA.

XX

AC AAY71560;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant NiAext.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

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PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -

XX

PS Example; Page -; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of
 CC all central nervous system (CNS) myelin material with which it is
 CC natively associated. Nogo proteins and fragments displaying neurite
 CC growth inhibitory activity are used in the treatment of neoplastic
 CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
 CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
 CC neuroma, oligodendroglioma, menangioma, neuroblastoma or retinoblastoma
 CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
 CC diseases. Therapeutics which promote Nogo activity can be used to treat
 CC or prevent hyperproliferative or benign dysproliferative disorders e.g.

Db 397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDDSSRAYITCASFT-SATESTTA 455
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 Qy 643 PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702
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 Db 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E 753
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 Job time : 84.555 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 28.5792 Seconds
 (without alignments)
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Title: US-09-830-972-29
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

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 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
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 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	931	15.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	787.5	13.3	776	2	US-08-700-607-5	Sequence 5, Appli
3	705	11.9	356	2	US-08-700-607-6	Sequence 6, Appli
4	688	11.6	208	2	US-08-700-607-7	Sequence 7, Appli
5	671	11.3	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.5	9.1	168	4	US-09-149-476-563	Sequence 563, App
7	513	8.7	241	2	US-08-700-607-3	Sequence 3, Appli
8	316	5.3	8991	4	US-08-714-741-32	Sequence 32, Appl
9	285	4.8	92	4	US-09-149-476-411	Sequence 411, App
10	276.5	4.7	1786	3	US-08-973-462-8	Sequence 8, Appli
11	267.5	4.5	1601	4	US-09-345-473E-40	Sequence 40, Appl

12	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
13	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
14	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
15	256	4.3	1780	3	US-08-994-570-5	Sequence 5, Appli
16	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
17	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
18	237.5	4.0	688	3	US-09-141-047-8	Sequence 8, Appli
19	237.5	4.0	1270	4	US-07-757-022B-44	Sequence 44, Appl
20	237.5	4.0	1311	4	US-07-757-022B-42	Sequence 42, Appl
21	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, App
22	237.5		1314	4	US-07-757-022B-50	Sequence 50, Appl
23	237.5	4.0	1320	4	US-07-757-022B-46	Sequence 46, Appl
24	237.5	4.0	1320	4	US-07-757-022B-60	Sequence 60, Appl
25	237.5	4.0	1354	4	US-07-757-022B-48	Sequence 48, Appl
26	237.5	4.0	1361	4	US-07-757-022B-40	Sequence 40, Appl
27	237.5	4.0	1363	4	US-07-757-022B-52	Sequence 52, Appl
28	237.5	4.0	1404	4	US-07-757-022B-2	Sequence 2, Appli
29	237.5	4.0	1404	4	US-07-757-022B-62	Sequence 62, Appl
30	234.5	4.0	941	4	US-07-757-022B-14	Sequence 14, Appl
31	234.5	4.0	1022	4	US-07-757-022B-84	Sequence 84, Appl
32	234.5	4.0	1038	4	US-07-757-022B-74	Sequence 74, Appl
33	234.5	4.0	1049	4	US-07-757-022B-58	Sequence 58, Appl
34	234.5	4.0	1140	4	US-07-757-022B-104	Sequence 104, App
35	233.5	3.9	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
36	226.5	3.8	630	3	US-08-973-462-9	Sequence 9, Appli
37	225	3.8	783	6	5231168-2	Patent No. 5231168
38	221	3.7	1087	4	US-09-914-259-12	Sequence 12, Appl
39	221	3.7	2482	4	US-09-252-991A-16967	Sequence 16967, A
40	220	3.7	1481	2	US-08-616-844-40	Sequence 40, Appl
41	220	3.7	1481	2	US-08-599-654-40	Sequence 40, Appl
42	220	3.7	1481	3	US-08-944-868A-40	Sequence 40, Appl
43	220	3.7	1400X7		-08-944-423A-40 GAKRH	Sequence 40, Appl
44	220	3.7	1481	3	US-08-944-496-40	Sequence 40, Appl
45	216.5	3.7	1848	3	US-08-296-791-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304


```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Query Match          13.3%; Score 787.5; DB 2; Length 776;
Best Local Similarity 31.9%; Pred. No. 3.1e-40;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

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Db      141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAAYKYIDIT 200

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Db      404 SSAESGD-----SEIELVSEDPMAAEDALPSGYVSFGHVGGPPPPSP 444

Qy      869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921
      : || : | : : | : : | : | | | | | |
Db      445 ASPSIQYSILREEREAE LDESELI IESCDASSAS-----EESPKREQDSPPMKPSALD 496

Qy      922 DF-----SKNGSATSKVLL-----LPPDV SALGHTQAEIESIVKP 956
      | : | | | | | | | | | | | | | | | |
Db      497 AIREETGVRAERAPSRRLAEPGSFLDYPSTEPQGPPELPPGDGAL-----EPETPMLP 551

Qy      957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001
      : | : : ||: | : | | | | | | | | | |
Db      552 -----RKPEEDSSSNQSPAATKGPGPLGPGAPPPLLF---LNKQKAIDLLYWRDIK 599

Qy      1002 KTG VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1061
      : ||: ||: | | | | | | | | | | | | | | | | | | | | | | | |
Db      600 QTGIVFGSFLLLLSLTQFSVSVVAYLALALALSATISFRIYKSVLQAVQKTDEGHPFKA 659

Qy      1062 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1121
      || | | : : | : ||:: : | | : || | | | | | | | | | | | | | | |
Db      660 YLELEITLSQEIQKYTDCLQFYVNSTLKE LRRLFLVQDLVDLSLKFAVLMWLLTYVGALF 719

Qy      1122 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
      || | | | | : : | : ||: ||: | | | | | | | | | | : : : | | | | | | |
Db      720 NGLTLLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 776

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RESULT 3

US-08-700-607-6

; Sequence 6, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

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; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

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Query Match          11.9%; Score 705; DB 2; Length 356;
Best Local Similarity 42.6%; Pred. No. 1.2e-35;
Matches 168; Conservative 55; Mismatches 86; Indels 85; Gaps 11;

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Qy      803 EVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFS DSSPIEIIDEFPTLISS 862
      : | | : : | | : : | | : | : | | | | : : | : :
Db      30 QYSILREEREAE L DSELI ---IESCDASSASEESPKRE---QDSPPMK-----PSALDA 77

Qy      863 KTDFSFKLAREYTDLEVSHKSEIANAPDGAGSL---PCTELPHDLSLKNIQPKVEEKISF 919
      | | | : : : : | | | | | | | | | | | | | | | |
Db      78 -----IREETGVRAEERAPSRRGLAEPGSFLDYPSTE-----PQPGPE----- 115

Qy      920 SDDFSKNGSATS K V L L L P P D V S A L G H T Q A E I E S I V K P K V L E K E A E K K L P S D T E K E D R S P S 979
      | | | | | | | | | | | | | | | | | | | | | | |
Db      116 -----LPPGDGAL-----EPETPMLP-----RKPEEDSSSNQSPA 145

Qy      980 A-----IFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLT VFSIVS 1024
      | : | | | : | | | : | | | | | | | | | | | | | |
Db      146 ATKGPGLPGGAPPPLLF---LNKQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVS 202

Qy      1025 VTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH 1084
      | | : | | | | | | | | | | | | | | | | | | | | :
Db      203 VVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFY 262

Qy      1085 VNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERH 1144
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Db      263 VNSTLKE LRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLLMVVSMFTLPVVYVKH 322

Qy      1145 QAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
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Db      323 QAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356

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RESULT 4
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708

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; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

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Query Match          11.6%; Score 688; DB 2; Length 208;
Best Local Similarity 67.5%; Pred. No. 5.9e-35;
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

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Qy      988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 1047
      | : : ||||| : || : || : | || ||| || : || | | ||||| | :
Db      18 KSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVSVVAYLALAALSATISFRIYKSVL 77

Qy     1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
      || : || : ||||| : |||| | : : | : ||| : : : || | : ||||| || |||||
Db      78 QAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKF 137

Qy     1108 AVLMMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
      ||||| : ||||| ||||| : || : || : || : || : ||||| |||| : : : ||||
Db     138 AVLMMWLLTYVGALFNGLTLLLMVVSMTFLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQ 197

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[illegible]

RESULT 6

US-09-149-476-563

; Sequence 563, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,618

EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,503

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
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; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          9.1%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 4.2e-26;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;
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Qy      1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 1072
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Db      1 MLLSLAAPSVISVVSYLIALALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      1073 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 1132
          | |:|: |:| :| : ||||: ||||| || ||: ||||: |||: ||||| :
Db      61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSKLAVFMWLMITYVGAVFNGITLLILAE 120
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Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178
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 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIKKA 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: THP1NOB01
 ; CLONE: 31870

US-08-700-607-3

Query Match 8.7%; Score 513; DB 2; Length 241;
 Best Local Similarity 47.7%; Pred. No. 4e-24;
 Matches 102; Conservative 37; Mismatches 55; Indels 20; Gaps 1;

Qy 963 AEKKLPSDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022
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Db	20	AEPSAPGGGGSPGACPALGTKSCSSCAVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSV	79
Qy	1023	VSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSAL	1082
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Db	80	ISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM	139
Qy	1083	GHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFITYVGALFNGLTLLILALISLFSVPVIYE	1142
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Db	140	VHINRAKLIIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFNGITLLILAELLI XSVPIVYX	199
Qy	1143	RHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRK	1176
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Db	200	KY-----KVPSKTPWNROK	213

RESULT 8

US-08-714-741-32

; Sequence 32, Application US/08714741

Patent No. 6500613

; GENERAL INFORMATION:

APPLICANT: Briles, David E.

; APPLICANT: McDaniel, Larry S.

; APPLICANT: Swiatlo, Edwin

; APPLICANT: Yother, Janet

; APPLICANT: Crain, Marilyn J.

; APPLICANT: Hollingshead, Susan

; APPLICANT: Tart, Rebecca

; APPLICANT: Brooks-Walter, Alexis

; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF.

7 TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES.

; TITLE OF INVENTION: PORTIONS AND PRODUCTS

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; NUMBER OF SEQUENCES: 47
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; CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.

; STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.

ZIP: 10036

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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;      COMPUTER:  IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,741

; FILING DATE: 16-SEP-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

NAME: Frommer Esq., William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454312-2460

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

; INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:


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;      LENGTH:   8991 amino acids
;      TYPE:     amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  amino acid
US-08-714-741-32

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Query Match 5.3%; Score 316; DB 4; Length 8991;
Best Local Similarity 21.4%; Pred. No. 8.4e-10;
Matches 248; Conservative 138; Mismatches 479; Indels 296; Gaps 52;

QY	6	QSPLVSSSDSP-PRPQPAFKYQF-VREPEDEEEEEEEDEDEDELEE--LEVLERKPA	61
Db	7193	EAPAEQPKPAPAPQAPAPAPKPEKPAEQPKPEKTTDDQQAEDYARRSEEEYNRLTQQQP	7252
QY	62	GLSAAPVP-----TAPAAG-----APLMDF	81
Db	7253	AEKPAPAPKTGWKQENGWYFYNTDGSMEQAGQYRAAAEGDLAAKQAELEKTEADLKKA	7312
QY	82	GNDFVPPAPRGLPAAPPVAPERQPSWDPSVSTVPAPSPLSAAAVSPSKLPED---DE	138
Db	7313	VNEPEKPAPAPETPA--PEAPAEQPK--PAPAPQAPAPKPEKPAEQPKAEKTTDDQQAEE	7368
QY	139	PPAR-----PPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXX	189
Db	7369	DYARRSEEEYNRLTQQQPPKAEKPAPAPKPEQAPAPAPKNSKGEQAEQYRSAAGGDLAAKQ	7428
QY	190	XKI---MDLKEQPGNTISAGQEDFPSVLLET-AASXPSLSPLSAAFSKEHEYLGNLSTV	244
Db	7429	VELEKTEADLKK-----AVNEPEKPAPAPETPAPEAPAEQPKPAPAPQ-----	7471
QY	245	LPTEGTLQENVSEASKEVSEKAKTLLIDRLTEFSELEYSEMGSFSVSPKAESAVIVAN	304
Db	7472	-PAPAPKPEKPAEQPK--AEKPADQQAEDYDRRSEEEYNRL--TQQQPPKAEKPAPAPQ	7526
QY	305	PREEI-----IVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNE	357
Db	7527	PEQPAPAPKSLKEIDESDSEDYVKEGFRAPLQSELDKQAKLSKLEEL-----SDKIDE	7580
QY	358	KRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQ	417
Db	7581	LDAEI-AKLEKDVEDFK-----XSDGEQAGQYLAAAEEDLIAKKA---ELEQ	7623
QY	418	TNHEKDESSNDDTSFPS---TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTS	474
Db	7624	T--EADLKKA VNEPGKPAPAPAE-----TPAPEAPAEQPK-----PAP	7660
QY	475	ENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYV--TTDNLTKVTEEVVA--	530
Db	7661	ETPAPAPKPEKPAEQPKPEK-----PADQQAEDYARRSEEEYNRLTQQQPAPA	7709
QY	531	-----NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP	584
Db	7710	QKPEQPAKPEKPAEEPTQPEKDAEIAKLE-KNVEYFKKTDAEQTEQYLAAAEKDLADKKA	7768
QY	585	SFEESEA-----TPSPV-LPDI VMEAPLNSAVPSAGASVIQPSSSPLEAS	628

Db 7769 ELEKTEADLKKAVNEPEKPAEETPAPAPKPEQPAEQPKPAPAPQP-APAPKPEKTTDDQQA 7827

Qy 629 SVNYESIKHEPENPPPYEEAMSVSLKVSGIKEE----IKEPENINAALQETEAPYISIIAC 684
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Db 7828 EEDYARRSEEEYNRLPQQQPPKAEKPAPAPKPEQPVPAEXPEN-----PAPAPKPAXAP 7881

Qy 685 DLIKETKLSAEPAPPDFSDYSEMAKVEQPV-----PDHSELVEDSS-----PDS 727
:| : : :| | :| | :| | :|

Db 7882 QPLKPEEPAEQPKPE-----KPEEPAGQPEPEKPDDQQAGEDYARRSGGEYNRFPQQ 7933

Qy 728 EPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGG----- 781
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Db 7934 QPPKAEKPAPAP----KPEQVPVAPKTL-----KKAKLAGAKSKAATKKAEL 7977

Qy 782 KPYLESFKLSLDNTKDTLLP-----DEV-----STLSKK-EKI PLQMEELSTAVYSNDD 829
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Db 7978 EPELEKAEAELENLLSTLDPEGKTQDELDKEAAEAELNKKVEALPNQVSELEEELSKLED 8037

Qy 830 LFISKEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLARE----YTDLEVSHKSEI 885
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Db 8038 NL--KDAETNNVEDY-----IKEGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 8088

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI--SFSDDFSKNGSATSXVLLLPDVSAL 943
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Db 8089 TPPPEAPAEQPKPEKPAE-ETPAPAPKPEKSADQQAEDYARRSEEEYNRL----- 8138

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRD---I 1000
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Db 8139 --TQQQ-----PPK-----AEKPAPAPAPKPEQAPAPAKSRGLATKKKLNLAELIALL 8186

Qy 1001 KKTGV-----VFGASLFLLLS 1016
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Db 8187 KKLGLEPGLKAGAGLGNLLS 8207

RESULT 9

US-09-149-476-411

; Sequence 411, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650

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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          4.8%; Score 285; DB 4; Length 92;
Best Local Similarity 57.1%; Pred. No. 9.8e-11;
Matches 52; Conservative 20; Mismatches 19; Indels 0; Gaps 0;
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Qy      1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 1138
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Db      2 NAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMITYVGAVFNGITLLILAELLIFSVP 61

Qy      1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169
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Db      62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
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RESULT 10

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US-08-973-462-8
; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
US-08-973-462-8
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Best Local Similarity 20.1%; Pred. No. 2.2e-08;
Matches 232; Conservative 201; Mismatches 471; Indels 249; Gaps 50;
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Qy      30 EPEDEEEEEEEEEDEDEDLEE-----LEVLERKPAAGLSAAPVPTAPAAGAPLMDFGN 83
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Db      228 EESVEENDEESVEENVEENVEENDDGSGVASSVEESIASSVDESIDSSIEENVAPTVE--- 284

Qy      84 DfVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPAR- 142
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Db	285	EIVAPS-----VVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAEN	338
Qy	143	----PPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQ	198
Db	339	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	398
Qy	199	PGNTISAGQEDFPSVLLETAAS-----XPSLSPLSAASFKEHEYLGNLSTVLPT-EGTL	251
Db	399	VAENV--EESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESV	455
Qy	252	QENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVI-----VANP	305
Db	456	EENVEESVAENVEESVAENVEESVAENVEESVAE-NVEESVAENVEESVAENVEESVAEN	514
Qy	306	REEIIVKNKDE----EEKLVSNNILHX-----QQELPTALTCLKVKED-----EVV	346
Db	515	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	574
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYA-----DFKPFERVWEVKDSKEDSDMLAAGGKIESN	401
Db	575	VAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEES-----VEEN	626
Qy	402	LESKVDKKCFADSLEQTNHE--KDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATE	459
Db	627	VEESV-----AENVEESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVA----PSVVE	677
Qy	460	SIATNIFPLLEDPTSENXTDE--KKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVT	517
Db	678	SVA----PSVEESVEENVEESVAENVEESVAENVEESVAENVEES---VAENVEEIVAPT	730
Qy	518	TDNLTKVT-EEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTS--EVMQ	573
Db	731	VEEIVAPTVEEIVAPSVVESVAPS-VEESVEENVEESVAENVE-ESVAENVEESVAENVE	788
Qy	574	ESLYPAAQ--LCPSFEESEATPSPVLPDI VMEAPLNSAVPSAGASVIQPSSSPLEASSVN	631
Db	789	ESVAPTVEEIVAPSVEESVA-PS-----VEESVAENVATNLSNLLSNLLGGIETEEIK	841
Qy	632	YESIKHEPENPPP-----YEEAMSVSLKV-SGIKEEIKE---PENINAALQETEA	677
Db	842	-DSILNEIEEVKENVVTILENVEETTAESVTTFSNILEEIQENTITNDTIEEKLEELHE	900
Qy	678	PYISIA-----CDLIKETKLSAEPAPDFSDYSEMA--KVEQPVPDHSSELVED	722
Db	901	NVLSAALENTQSEEEKKEVIDVIEEVK--EEVATTLIETVEQAEEKSANTITEIFENLEE	958
Qy	723	SSPDS-----EPVDLFSDDSI PDVPQKQDETVM LVKESLTET-----	759
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Qy	760	-----SFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK	810
Db	1019	ENLLTGMRFSIETSI VIQSEEKVDL-----NENVVSSILDNIENMKEGLL-NKLENISST	1072
Qy	811	E-----KIPLQME-----LSTAVYSNDDL F-----	831

Db 1073 EGVQETVTEHVEQNVYVDVDVPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESDVITVEE 1132

Qy 832 -----ISKEAQIRETETFSDSPIEIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIA 886
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Db 1133 IKDEPVQKEVE-KETVSIIEEMEENIVDVLEEEKEDLTDKMIDAVEESIEISSDSKEETE 1191

Qy 887 NAPDGAG--SLPCTELPHD-----LSLKNIQPK-VEEKISFSDDFSKNGSATS SKVL 934
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Db 1245 ---EETQELNEVEAD---LIK DMEKLKELEKALS EDSKEI IDAKDDTLEK VIEEEHDITT 1298

Qy 990 SVVDLLYWRDIKK 1002
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Db 1299 TLDEVVELKDVEE 1311

RESULT 11

US-09-345-473E-40

; Sequence 40, Application US/09345473E

; Patent No. 6558903

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin

; TITLE OF INVENTION: No. 6558903e1 Kinases and Uses Thereof

; FILE REFERENCE: 35800/183781

; CURRENT APPLICATION NUMBER: US/09/345,473E

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 40

; LENGTH: 1601

; TYPE: PRT

; ORGANISM: C. elegans

US-09-345-473E-40

Query Match 4.5%; Score 267.5; DB 4; Length 1601;

Best Local Similarity 20.5%; Pred. No. 6.8e-08;

Matches 229; Conservative 134; Mismatches 376; Indels 377; Gaps 56;

Qy 29 REPEDEEEEEEEEE-----EDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGA 76
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Db 462 RAKEEEERIREEAEIKEELRLRAEAKEKEKERLEK-ERLEK KAAAAAANPNP TP----- 515

Qy 77 PLMDFGNDFVPPAPRGP-----LPAAPPVAPE-----RQPSWDPS-PVS--STVPAPSP 122
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Db 516 -----IPPTPATPHSSAQQQPIPPPLSTQTS AEIQQSAQQPSVPVTMIANI PAMSP 566

Qy 123 LSA---AAVSPSK----LPEDDEPPARPPPPPPASVSPQAEPVW---TPPAPAP--AAPP 170
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Db 567 TSAQPQPVL SPTSAAVPVPTTMIHVPK PSEI PVQNVATTAAPVAANNVPPSPAPFKTE DI 626

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Db 627 QTPTLAQ-----NTVPR TISTDASGLVINTPASIASPSPAPS 663

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| | : : | | : : | : | : : | : : : :
Db 780 NSDGKKGVGTKLAT--VLDPNSTEPPTITAVMPKD---SSAATASNTKPKIEI----- 827

Qy 369 EYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESN 428
| : : | : : : : : : : : : : : :
Db 828 -----EKTPPTRDASQE-----PNNVQVTNVRKVSQESN 856

Qy 429 DDTSPSTPEGIKDRSGAYITCAPFN-----PAAT---ES 460
: | | | | : | | : | | :
Db 857 AE-SVQSIP-----RPGGIIVMSPTNQDSAPPPTGAAAKPSRFQVTKSADPIATPISSS 910

Qy 461 IAT-NIFPILLEDPTSENXTDEKKIEEK-KAQIVTEKNTSTKTSNPFVAAQDSETDYVTT 518
| : | : : | | | | : | : | : : | : : : :
Db 911 ISTATVIPIVA-ATPTNITSEPVIVQPIITAQVITHLATPSPVSHSL---SSNSSPSATTH 966

Qy 519 DNLTKVTEEVVANMP-EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLY 577
| : : : : : : | : | | : : | :
Db 967 SNMSSI--QSTTSVPGRRFTVQPVSA-ESGISSSISTPHPEPT----- 1007

Qy 578 PAAQLCPSFEESEATPSPVLPDIVMEAPLNSAV-----PSAGASVIQPSSSPLEASSVNY 632
| | | | | : | : : | | | : : | : :
Db 1008 PAITSCP-----PPVPSVPPVVSNGTLNLEVAPKQTPSATNQNVDTQHSSSTASTATL 1060

Qy 633 ESIKHEPEN-----PPPYEEAMSVS-----LKVSGIKEEIKEPENINAA 671
: | | : : : : : : : : : :
Db 1061 --VSETPATVHVTPISVPAPVQEPLVIDHHSVDLTQLDSELRKVSGVSHS-ASPSTVVES 1117

Qy 672 LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVD 731
| : | : : : | : : : : : : : :
Db 1118 LTSMTPTIPLACQTV-PASIGQAPAVIAAAHA-----AS 1151

Qy 732 LFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS 791
| : | : | : | : | : : | : | : : : :
Db 1152 LIPNASVPQSPSRLD-----AETGLAGL-----HEKLEAL-----KME 1184

Qy 792 LDNTKDTLLPDE---VSTLSKKEKI PLQ-----MEELSTAVYSNDDLFI SKEAQIRET-- 841
| : | : : : | : : | : : : : : : : : :
Db 1185 QDRRED--MGDDAIGTTTTD GKDEI PIDTLKGLAEALGKVIHADG-----RETP 1232

Qy 842 -----ETFSDSPIEII-----DEFPTLISSKTDSFSKLAREYTDLEVS--HKSEIANAP 889
: | : : : | : : | : | : | : : : : :
Db 1233 MPPDHPDLTDASTQQLISPSNPDLVLTMTSSAVEGSASSTMI EDIDASTSAVDASMMNSMP 1292

Qy 890 DGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGHTQAE 949
| | : : : : : : | : : : : : :
Db 1293 PGA-----QNSTDQI PAAMTLSMDQECAQSMTSSITR-----NTTGTKLAT 1333

Qy 950 IESIVKPKVLEKEAEKKLPSTDEKEDRSPSAIFSAD 985

Db 1334 FENL-----ETALSSTLGTHIRQPNAPSSRD 1359

RESULT 12

US-08-978-277A-4

; Sequence 4, Application US/08978277A
; Patent No. 6582956
; GENERAL INFORMATION:
; APPLICANT: Gelman, Irwin H.
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,277A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/665,401
; FILING DATE: 18-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: A30558 - 165/34008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1596 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

US-08-978-277A-4

Query Match 4.5%; Score 265; DB 4; Length 1596;
Best Local Similarity 21.3%; Pred. No. 9.6e-08;
Matches 232; Conservative 145; Mismatches 422; Indels 288; Gaps 47;

QY 2 EDLD--QSPLVSSSDSPRPQPAFKYQFVREPEDE-----EEEEEEEEEEDEDEDLEELEV 54

Db	620	EELEKVKSATLSSTDST-----VSEMQDEVKTVGEEQKPEEPKRRVDTSVSWEA	668
Qy	55	LERKPAAGLSAAPVPTAPAAGAPL-----MDFGNDFVPPAPR-----	91
Db	669	LICVGSSKKRARKASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQDQAQGS	728
Qy	92	-GPLPAAPPVAPERQPSWDPSVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPAS	150
Db	729	SSPEPAGSPSEGEVSTWE-----SFKRLVTPRKK---SKSKLEEKAEEDSS--VEQLSTE	778
Qy	151	VSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAG----	206
Db	779	IEPSREESWV-----SIKKFIPGRRKKRA-----DGKQEATVEDSGPVEI	819
Qy	207	QEDFPSVLLETAASXPSLSPLSAASFKEHEYL---GN-----LSTVLPTEGTLQENVSE	257
Db	820	NEDDPNV-----PAVVPLSEYNAVEREKMEAQGNTELPQLLGAVYVSE-----E	863
Qy	258	ASKEVSEKAKTLLID--RDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIIVKNKD	315
Db	864	LSKTLVHTVSVAVIDGTRAVTSVEERSPSWISASVT-EPLEHTAGEAMPPEEVTEKDII	922
Qy	316	EEEKLVSNNILHXQQELPTALTKLVKE-----DEVVSSEKAKDSFNEKRVAVEAPMREEY	370
Db	923	AEETPV-----LTQTLPEGKDAHDDMTSEVDFTS-----EAVTATET	960
Qy	371	ADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDD	430
Db	961	SEALRTEEVTASGAETTDMVSAVSQLTDS-----PDTTEEATPVQEVESGVLD	1010
Qy	431	TS-----FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDEK	481
Db	1011	TEEEERQTQAILQAVADKVKEES-----QVPATQTVQRTGSKALE-----KVE	1053
Qy	482	KIEEKKAQIVTEKNTSTKTSNPPFFVA-----AQDSETDYVTTDNLTKVTEEVVANMPEGL	536
Db	1054	EVEEDSEVLASEKEKDVMPKGPVQEAGAEHLAQGSETGQAT-----PESL	1098
Qy	537	TPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPV	596
Db	1099	-----EVPEVT-ADVDPVATCQVIKLOQLMEQAVAPESS--ETLTDSETNGSTP	1144
Qy	597	LPD-----IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMS	650
Db	1145	LADSDTADGTQQDETIDSQDSKATAAVRQSQVTEEEAATAQKEEPSTLPNNVPAQE----	1200
Qy	651	VSLKVSIGIKKEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVE	710
Db	1201	-----EHGEEPG--RDVLEPTQQELTAAAVPVLAKTEVGQEGEVDWLD-GEKVKEE	1248
Qy	711	QPVPDHSELVEDSSPDSE-PVDLFSDDSI PDVPQKQD-ETVMLVKESLTETSFESMIEYE	768
Db	1249	QEVFVH-----SGPNSQKAADVTDSEVMGVAGCQEKESTEVQSLSLEEGEMETDVEKE	1302
Qy	769	NKE-KLSALPPEG-----GKPYLESFKLSLDNTK-----DTLLPDEVSTL	807

Db	1303	KRETKEPQVSEEGEQETAAPHEGTYGKPVLTLDMPSSERKGALGSLGGSPSLPDQ----	1358
Qy	808	SKKEKIPLOMEELSTAVYSNDDLFISKEAQIRETETFSDS--SPIEIIIDE--FPTLISSK	863
		: : : : : :	
Db	1359	DKAGCIEVQVQSLDTTQTAQAEV---EKVIETVVISETGESPECVGAHLLPAEKSSA	1413
Qy	864	TDSFSKLAAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFS---	920
		: : : : : : :	
Db	1414	TGGHWTLQHAEDTVPLGPESQ-----AESIPIIVTPAPES--TLHPDLQGEISASQRE	1464
Qy	921	-----DDFSKNGSATSQVLLPPDVSAHGHTQAEIESIVKPKVLEKEAEKKLP	968
		: : : : : :	
Db	1465	RSEEDDKPDAGPDADGKESTAIEKVLKAEPEILELESKNKIVLNVIQTAVDQFARTETA	1524
Qy	969	SDTEKED	975
		:	
Db	1525	PETHAYD	1531

5180808-2

; APPLICANT: RUOSLAHTI, ERKKI I.

;SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN

; NUMBER OF SEQUENCES: 4

; APPLICATION NUMBER: US/07/441,179

;SEQ ID NO:2:

5180808-2

Best Local Similarity 20.1%; Pred. No. 2.1e-07;

Matches 253; Conservative 180; Mismatches 479; Indels 345; Gaps 58;

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Db 910 ENITQTSREIVISERLGEPNYGAEIRGFST---GFPLEEDFSGDF-----REYSTVSHP 960

Qy 100 VAPE-----RQPSWDPSPVSTV-----PAPSPLSAAAVSPSKLP-EDDEP 139

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Db 961 IAKEETVMMEGSGDAAFRDTQTSPSTVPTSVHISHISDSEGP-SSTMVSTSAFPWEEFTS 1019

Qy 140 PARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEOP 199

		:									::	::	::		
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Db 1020 SAEGSGEQLVTVSSSVVPVL-----PS--AVQKFSGTASSII-----DEGL 1058

Qy 200 GNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLP----- 246

[illegible]

Db 1059 GEVGTVNEIDRRSTILPTAEVEGTKAPVEK---EEVKVSGTVSTNFPQTIEPAKLWSRQE 1115

Qy 247 -----TEGTLQENVSEASKEVSEKAKTLLIDRDL---TEFSELEYSEMGSSF 290

Db 1116 VNPVRQEIESETTSEEQIQEEKSFESPQNSPATEQTIFDSQTFTELTETKTTDYSVLTTKK 1175

Qy	291	SVSPKAESAIVANPREEII VKNKDEEEKLVLS-----NNILHXQQELPTALTCLKVKED	343
Db	1176	TYSDDKEM-----KEEDTSLVNMSTPDPDANGLESYTTLPEATE---KSH	1217
Qy	344	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG-GKIESNL	402
Db	1218	FFLATALVTESIPAHEVVTDSPIKKEEST-KHFPKGMRTIQESDTELLFSGGLSGSEEVL	1276
Qy	403	ESKVDKKCFADSLEQTN-----HEKDSSES-SNDDTSFPSTPEGIKDRSGAYITCAPFNP	456
Db	1277	PTLPTESVNFTEVEQINNTLYPHTSQVESTSSDKIEDFNRMENVAKEVGPLVSQTDIFEG	1336
Qy	457	ATESIATNIFPLLEDPTSEN-----XTD-----EKKIEEKKAQIVTEKNTS	497
Db	1337	SGSVTSTTLIEILSDTGAEGPTVAPLPFSTDIGHQPQNQTVRWAAEIIQTSRPQTITEQDSN	1396
Qy	498	TKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKI	557
Db	1397	KNSSTA EINETTTSSD TFLARAYGFEMAKEFVTSAPK--PSDLYYEPSGEGSGEV-----	1449
Qy	558	AYETKMDLVQ-----TSEVMQESLYP-----AAQLCPSFESEATPSPVLPDIVMEAP	605
Db	1450	-----DIVDSFHTSATTQATRQESSTTFVSDGSLEKHPEVPSAKAVTADGFPTVSVMLP	1503
Qy	606	LNSAVPSAGASVIQSSSPLEASSVNYESI KHEPENPPPYEEAMSVSLKVSIGIKEEIKEP	665
Db	1504	LHSE-----QNKSSPDPTSTLS-NTVSYERSTDGSFQDRFR-EFEDSTLKPNRKKP	1552
Qy	666	ENINAALQETEAPYISIIACDLIKETK-----LSAEPAPDF-SDYSEMAKVEQPVPD	715
Db	1553	-----TE---NIIIDLKEDKDLILTITESTILEILPELTS DKNTIIDIHTKPV	1599
Qy	716	HSELVE-----DSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIE----	766
Db	1600	YEDILGMQTDIDTEVPSEPHD-SNDESNDSTQVQEIYEA AVNLSL TEETFEGSADVLAS	1658
Qy	767	-----YENKEKL-----SALPPEGGKPYLESFKLSLDNTKDTLLPDEVST	806
Db	1659	YTQATHDESMTYEDRSQLDHMGFHTTGIPAP-----STETELDVLLPTATSLP	1707
Qy	807	LSKKEK--IPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPI----EIIDEFP TLI	860
Db	1708	IPRKSATVIP-EIEG IKA EAKALDDMF-----ESSTLS DGQAIADQSEII---PTL-	1754
Qy	861	SSKTDSFSKLAREYTDLE-----VSHKSEIANAPDGAGSLPCTELPH	902
Db	1755	----GQFERTQEEYEDKKHAGPSFQPEFSSGABEALVDHTPYLSIATTHLMDQSVTEVPD	1810
Qy	903	DLSLKNIQPKVEEKISFSDDFS KNGSAT-SKVL LPPDV SALGHTQ-----	947
Db	1811	VMEGSNPPYYTDTTLAVS-TFAKLSSQTPSSPLTIYSGSEASGHT EIPQPSALPGIDVGS	1869
Qy	948	-----AEIESIVKP---KVLEKEAEKKLP SDTE---KEDRSPSAIF SADLG	987
Db	1870	SVMSPQDSFKEIHVNI EATFKPSSEEY LHITEPPSLSPDTKLEPSEDDGKPELLEEMEAS	1929

Qy 988 KTSVV-----DLLYWRDIKKTGVVFGASLFLLLSL---TVFSIVSVTAYIALA----- 1032
 | : : : : | | | : : : : : : : : | |
 Db 1930 PTELIAVEGTEILQDFQNKTDGQVSGEAIKMFPTIKTPEAGTVITTADEIELEGATQWPH 1989
 Qy 1033 LLSVTISFRIYKGV-----QAIQKSDEGHP-FRAYL----ESEVAISEELV 1074
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 Db 1990 STSASATYGVEAGVVPWLSPQTSERPTLSSSPEINPETQAALIRGQDSTIAASEQQV 2046

RESULT 14

US-08-769-309A-5

; Sequence 5, Application US/08769309A

; Patent No. 5741890

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/769,309A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5741890and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33451

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1780 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-769-309A-5

Query Match 4.3%; Score 256; DB 1; Length 1780;

Best Local Similarity 19.2%; Pred. No. 4e-07;

Matches 221; Conservative 163; Mismatches 419; Indels 348; Gaps 45;

Qy 1 MEDLDQSPLVSS--SDSPPRPQPAFKYQFV-----REPEDEEEEEEEEE----- 42
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Db 775 LEEKSEDSIAGSGVEHSTPDTEPGKEESWVSIKKFIPGRRKKRPDGKQEAPVEDAGPTG 834

Qy 43 -EDEDED-----LEELEVLERKPAAGLSA---APVPTAPAAGAPLMDFGNDFV--PPAP 90
 : : | | : : | : | | : | |

Db 835 ANEDDSVPAVVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMMAAA 894

Qy 91 RGPLPAAPPVAPERQPSWDPSVPS---STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP 147
 | : | | | : | : | : | : : | |

Db 895 VADGTRAATIIIEERSPSWISASVTEPLEQVEAEALLTEEVLEREVIAEEEPPTVTEPLP 954

Qy 148 PASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ 207
 : : | | : : :

Db 955 -----ENREARGDTVVSEA 968

Qy 208 EDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAK 267
 | | : | | | | : | : | : | | :

Db 969 ELTPEAV--TAA-----ETAGPLGSEEGTEASAAEETTEMVSAVSQLTLD 1010

Qy 268 TLLIDRDLTEFSELE-----YSEMSSFSVSPKAESAVIVANPREEII--VKN 313
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Db 1011 SPDTTEEATPVQEVEGGVPDIEEQERRTQEVLQAVAEEKVKEESQLPGTGGPEDVLQPVQR 1070

Qy 314 KDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNE-----KRVAVEAPMRE 368
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Db 1071 AEAE-----RPEEQAEASGLKKETDVVLKVDAQEAKTEPFTQGVVGTTP--- 1116

Qy 369 EYADFKPFERVWEVKDSKEDSDMLA-----AGGKIESNLESKVDDKKCFADSLE-QTNH 420
 : | : : | | : : | | : : | : | :

Db 1117 -----ESFEKAPQVTESESSELVTTCAETLAGVKSQ---EMVMEQAI PPDSVETPTDS 1168

Qy 421 EKBGESSNDDTSFPSTPE5X: GIKDRSGAYI-----TCAPFNPAATESIATNIFPLLE 470
 | | : | | : : : : | | | : :

Db 1169 ETDGSTPVADFDAPGTTQKDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPPAPSSSFVFQ 1228

Qy 471 DPTSENXTDEKKIEEKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVA 530
 : | | : | : | : | : | : | : :

Db 1229 EETKEQSKMEDTLEH-----TDKEVSVETVSIL-----SKTE--GTQEADQYADEKTK 1274

Qy 531 NMP--EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEE 588
 : : | | | : : | : : | : : | :

Db 1275 DVPFFEGL-----EGSID--TGITVSREKVTEVALKGEGTEEAECKDDALELQSH 1323

Qy 589 SEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPE----- 640
 : : | | | : : : : : | : | : | :

Db 1324 AKSPSPVEREMVVQ-----VEREKTEAEPHVNEEKLEHEIAVTVSEEVS 1369

Qy 641 -----NPPP---YEEAMSVSLKVSGIKEEIKEPENINAALQE 674
 : | | | | | : : | : :

Db 1370 KQLLQTVNVPIIDGAKEVSSLEGSPPPCLGQEEAVCTKIQV-----QS 1412

Qy 675 TEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLF- 733
 : | : | : | : | : | : | : | : | :

Db 1413 SEASFTLTAA--AEEKVLGETA---NILETGETLEPAGAHVLLEKSSEKNEDFAAHP 1466

Qy 734 SDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEK----- 773
 : : : | | : : : : | : | |

Db 1467 GEDAVPTGPDCAKSTPVIIVSATTKKGLSSDLEGEKTTSLKWKSDDEVDEQVACQEVKVS 1526

Qy 774 --SALPPEGKPYLE--SFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDD 829
 | | | | | | | : | : | | : | : : :
 Db 1527 AIEDLEPENGILELETKSSKL-VQNI IQTAVDQFVRT-----EETATEMLTSE- 1573

Qy 830 LFISKEAQI-----RETETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDL--E 878
 : : | : : | | : | | : : : : : | : :
 Db 1574 --LQTQAHVIKADSQDAGQETEKEGEEPQASAQDETPTSKEESESTAVGQAHSDISKD 1631

Qy 879 VSHKSEIANAPDGAGS-----LPCTE-----LPHD-----LSLKNI 909
 : | | : | | | | : | | : : : : :
 Db 1632 MSEASEKTMTVEVEGSTVNDQQLEEVVLPSEEEGGGAGTKSVPEDDGHALLAERIEKSLV 1691

Qy 910 QPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKE----- 962
 : | | : | | | | : | | | | | | | | | | hom
 Db 1692 EPKEDEKGGDDVDDPENQNSALA-----DTDASGGLTKESPD TNGPKQKEKEDAQEVEL 1744

Qy 963 AEKKLPDTEK 973
 | | : : : |
 Db 1745 QEGKVHSESDK 1755

RESULT 15

US-08-994-570-5

; Sequence 5, Application US/08994570

; Patent No. 6090929

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/994,570

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6090929and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33451

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-994-570-5

Query Match 4.3%; Score 256; DB 3; Length 1780;
Best Local Similarity 19.2%; Pred. No. 4e-07;
Matches 221; Conservative 163; Mismatches 419; Indels 348; Gaps 45;

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Qy      1 MEDLDQSPLVSS--SDSPPRPQPAFKYQFV-----REPEDEEEEEEEEE----- 42
      :|:  :  :  |  |  :|  :  :|  :  :|:  :|:  :|:  :|:
Db      775 LEEKSEDSIAGSGVEHSTPDTEPGKEESWVSIKKFIPGRRKKRPDGKQEQAPVEDAGPTG 834

Qy      43 -EDEDED-----LEELEVLERKPAAGLSA---APVPTAPAAGAPLMDFGNDFV--PPAP 90
      :|:  |  |  |  :  :|:  |  |  |  |  |  |  :  :  |  |
Db      835 ANEDDSDVPAVVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMAAAA 894

Qy      91 RGPLPAAPPVAPERQPSWDPSVPS---STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP 147
      |  :  ||  ||  :  :|  |  :  |  |  :  :  :|  ||  |
Db      895 VADGTRAATIIERSPSWISASVTEPLEQVEAEAALLTEEVLEREVIAEEEPPTVTEPLP 954

Qy     148 PASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ 207
      :  :|  |  :|:  :
Db     955 -----ENREARGDTVVSEA 968

Qy     208 EDFPSVILLETAASXPSPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAK 267
      |  |  :  ||  |  |  |  |  |  |  :  |  :|  ||  :
Db     969 ELTPEAV--TAA-----ETAGPLGSEEGTEASAAEETTEMVSAVSQQLTD 1010

Qy     268 TLLIDRDLTEFSELE-----YSEMGSSFSVSPKAESAVIVANPREEII--VKN 313
      :  :  :  |  :|  |  :  :  :  |  ||  :  |  :  :|  :
Db    1011 SPDTTEEATPVQEVEGGVPDIEEQERRTQEVQLQAVAEKVKEESQLPGTGGPEDVLQPVQR 1070

Qy     314 KDEEEKLVSNNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNE-----KRVAVEAPMRE 368
      :  |  :  :  :  |  ||  :|  |  :  :  :  |  |  |  |
Db    1071 AEAE-----RPEEQAEASGLKKETDVVLKVDAQEAKTEPFTQGKVVGQTTP--- 1116

Qy     369 EYADFKPFERVWEVKDSKEDSDMLA-----AGGKIESNLESKVDKKCFADSLE-QTNH 420
      :  ||  :  :|  :|  |  :  :  |  |  :  :  :  |  :|  |
Db    1117 -----ESFEKAPQVTESI ESSELVTTTCAETLAGVKSQ---EMVMEQAI PPDSVETPTDS 1168

Qy     421 EKDESSSNDDTSFPSTPE-----GIKDRSGAYI-----TCAPFNPAATESIATNIFPLLE 470
      |  |  :  |  |  :  :  :  :  :  :  |  |  |  |  :  :
Db    1169 ETDGSTPVADFDAPGTTQKDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPPAPSSSFVFQ 1228

Qy     471 DPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVA 530
      :  |  |  :  :|  |  :|  |  :  :  :  |  :|  :  :  :|
Db    1229 EETKEQSKMEDTLEH-----TDKEVSVETVSIL-----SKTE--GTQEADQYADEKTK 1274

Qy     531 NMP--EGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEE 588
      :|  ||  |  :  :  ||  :  :  |  :  :  |  :|  :
Db    1275 DVPPFFEGL-----EGSID--TGITVSREKVTEVALKGEGTEEAECKKDDALELQSH 1323

Qy     589 SEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPE----- 640
      :  :  ||  ||  :  :|  :  :  :  :  :  :  :  :  |  :  ||  |  :  :|
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Db 1324 AKSPSPVEREMVVQ-----VEREKTEAEPHVNEEKLEHETAVTVSEEVS 1369
 Qy 641 -----NPPP---YEEAMSVSLKVSGIKEEIKEPENINAALQE 674
 Db 1370 KQLLQTVNVPIIDGAKEVSSLEGSPPPCLGQEEAVCTKIQV-----QS 1412
 Qy 675 TEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLF- 733
 Db 1413 SEASFTLTAA--AEEKVLGETA---NILETGETLEPAGAHVLVEEKSSSEKNEDFAAHP 1466
 Qy 734 SDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKL----- 773
 Db 1467 GEDAVPTGPDCAKSTPVIVSATTKKGLSSDLEGEKTTSLKWKSDDEVDEQVACQEVKVS 1526
 Qy 774 --SALPPEGKPYLE--SFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDD 829
 Db 1527 AIEDLEPENGILELETKSSKL-VQNI IQTAVDQFVRT-----EETATEMLTSE- 1573
 Qy 830 LFISKEAQI-----RETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDL--E 878
 Db 1574 --LQTQAHVIKADSQDAGQETEKEGEEPQASAQDETPTSKEESESTAVGQAHSDISKD 1631
 Qy 879 VSHKSEIANAPDGAGS-----LPCTE-----LPHD-----LSLKNI 909
 Db 1632 MSEASEKTMTVEVEGSTVNDQQL EEVVLPSEEEGGGAGTKSVPEDDGHALLAERIEKSLV 1691
 Qy 910 QPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLEKE----- 962
 Db 1692 EPKEDEKGDDVDDPENQNSALA-----DTDASGGLTKESPD TNGPKQKEKEDAQLEVEL 1744
 Qy 963 AEKKLPSDTEK 973
 Db 1745 QEGKVHSESDK 1755

Search completed: January 22, 2004, 16:34:54
 Job time : 33.5792 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 32.1516 Seconds
(without alignments)
3523.514 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	787.5	13.3	776	2	A46583	neuroendocrine-spe
2	688	11.6	208	2	I60904	neuroendocrine-spe
3	671	11.3	267	2	A60021	tropomyosin-relate
4	528	8.9	2484	2	T26216	hypothetical prote
5	519.5	8.8	2607	2	T26215	hypothetical prote
6	340.5	5.7	222	2	T26213	hypothetical prote
7	331	5.6	7962	2	I38346	elastic titin - hu
8	325.5	5.5	5327	2	T13564	microtubule-associ
9	324.5	5.5	865	2	A47282	calcium-binding pr
10	320.5	5.4	873	2	A47283	calphotin - fruit
11	299.5	5.1	3488	2	T34418	hypothetical prote
12	299	5.0	3924	2	S37431	ankyrin 2, neurona
13	290.5	4.9	1274	2	T16251	hypothetical prote

14	289	4.9	2364	2	A56577	microtubule-associ
15	289	4.9	2464	1	QRMSPI	microtubule-associ
16	287.5	4.9	971	2	T19431	hypothetical prote
17	285.5	4.8	1621	2	A82255	hypothetical prote
18	278	4.7	1948	2	S00485	gene 11-1 protein
19	274	4.6	3507	2	T34513	hypothetical prote
20	272.5	4.6	1829	2	T24583	hypothetical prote
21	272.5	4.6	2361	2	T25752	hypothetical prote
22	271	4.6	2187	2	T30826	nascent polypeptid
23	270	4.6	1230	2	T22458	hypothetical prote
24	267.5	4.5	1851	2	T19964	hypothetical prote
25	263.5	4.4	2409	1	A60979	versican precursor
26	262.5	4.4	6642	2	T29757	protein UNC-89 - C
27	261	4.4	1558	2	B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	2	T42389	versican precursor
29	259.5	4.4	1828	2	A40115	microtubule-associ
30	258	4.4	1616	2	G64242	cytadherence-acces
31	257.5	4.3	5170	2	T15348	hypothetical prote
32	256	4.3	990	2	I51618	nucleolar phosphop
33	256	4.3	1634	2	T26517	hypothetical prote
34	255.5	4.3	1684	2	JW0057	gravin - human
35	253	4.3	1189	2	S56852	hypothetical prote
36	252.5	4.3	1224	2	T14007	microtubule-associ
37	252	4.3	4377	2	A55575	ankyrin 3, long sp
38	250.5	4.2	1824	1	QRHUMT	microtubule-associ
39	250.5	4.2	1830	2	A37981	microtubule-associ
40	248	4.2	1825	2	S13507	microtubule-associ
41	248	4.2	1890	2	T04556	hypothetical prote
42	248	4.2	3421	1	WZBEB6	367K tegument prot
43	246	4.2	1110	2	I51116	NF-180 - sea lampr
44	244.5	4.1	1029	2	T30351	mucin-like protein
45	243	4.1	1320	2	JC5630	TCOF1 protein - mo

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 13.3%; Score 787.5; DB 2; Length 776;
Best Local Similarity 31.9%; Pred. No. 3.1e-25;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

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Qy      588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY---- 632
      |  || | |||: :  | |:  | :  | :  ||:  | : |
Db      141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYKYIDIT 200

Qy      633 --ESIKHEPENPPPYEEA-----MSVSLKVGSIKEEIKEPENINAAL-----QET 675
      | :||: :: | |:  :|| | |:| | | :  :  : |
Db      201 RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKI IKDHLLLEEST 259

Qy      676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQPVDPHSELVED 722
      ||||  ||  :| |  ||: :  : : | : ::
Db      260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309

Qy      723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMLVKESLTETSF 761
      |||: |  |||  | : |  || : : ||:
Db      310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363

Qy      762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821
      : || | : : | :  || | | | : : :
Db      364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403

Qy      822 TAVYSNDDLFI SKEAQIRETETFS DSSPIEIIDEFP---TLISSKTDSFS----- 868
      :: | |  |||: | | : | ||
Db      404 SSAESGD-----SEIELVSEDPMAAEDALPSGVVSFGHVGGPPPPSP 444

Qy      869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921
      : || : |: : | : : | : | | | | |
Db      445 ASPSIQYSILREEREAE LDELII ESCDASSAS-----EESPKREQDSPMKPSALD 496

Qy      922 DF-----SKNGSATS K VLL-----LPPDV SALGHTQAEIESIVKP 956
      | : | |  |||  || | | : |
Db      497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQGPPELPPGDGAL-----EPETPMLP 551

Qy      957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001
      : | :  : ||: |  : | | | : |||||
Db      552 -----RKPEEDSSSNQSPAATKGPGLGPGAPPPLLF---LNKQKAIDLLYWRDIK 599

Qy      1002 KTG VVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1061
      : ||: ||: | || ||| ||: ||| || ||||| | : ||: ||: ||||| : |
Db      600 QTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKA 659

Qy      1062 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1121
      ||| | : |: | : ||: :  : || | : ||||| ||||| ||||| : |||||
Db      660 YLELEITLSQEIQKYTDCLQFYVNSTLKE LRRLFLVQDLVDLSLKFAVLMWLLTYVGALF 719

```

QY 1122 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKI PGLKRKAE 1178
|||:::||:|::||:| :|||| | ||| :: :||||||| || ||
Db 720 NGLTLLLMAVVSMTLPVVYVKHQAOIQYLGLVRTHINAVVAKI OAKI PGAKRHA E 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence revision 24-May-1996 #text change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: E

TKL

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C; Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 11.6%; Score 688; DB 2; Length 208;

Best Local Similarity 67.5%; Pred. No. 6.2e-22;

Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

Qy 988 KTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1047
 | : | : ||||| : | : | : | | | | : | | : | | | | | | | :

Db 18 KSQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 77

Qy 1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKF 1107

Db 78 QAVQKTDEGHPPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVODLVDSLKF 137

[illegible]

Db 138 AVLMWLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIO 197

Qy 1168 AKIPGLKRKAE 1178

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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Db 198 AKIPGAKRHAE 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

Qy	39	EEEEED-----EDEDLEEVLERKPA-----AGLSAAP-----	67
Db	1454	NQEEEDVVAELNFHPRIQRWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP--ERQPSW-----	108
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSVVSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEFPVVPQVQERIIP	1624
Qy	160	TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVL--LE	216
Db	1625	VEQAPTIPQRPPRAP-----KSELPKVAKPLD	1651
Qy	217	TAASXPSSLPLSA-----ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLL	270
Db	1652	DSKSRVRFAPLNIKLGRITYSEEQQKELVESLERPL-TIITQQKPPEKPTEDIG--ALSPL	1708
Qy	271	IDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQ	330
Db	1709	SPNTLAEYEEVPMMDMQS-----VPHSPQE-----KQEEIEALSEII-----	1745
Qy	331	ELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK--PFERVWEVKDSKE	387
Db	1746	EEPQAMKEVEKPVESAPEKDNESELEPEI-INEPIRRVLVETKIMGPGKSLNEDNDDDD	1803
Qy	388	D-SDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESS---NDDTSFPSTPEGIKD	442
Db	1804	DGSECLDSIGDLS---ERTIQR--FNSTIDDPISRRDSFSSISSFGDRQKFRTAIENIRQ	1858
Qy	443	RSGAYITCAPFNPAAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSN	502
Db	1859	-----DLLPFQSSVSQYLRSSNP-----SQQLLVTN-----	1885
Qy	503	PPFVAAQDSETDYVTNDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETK	562
Db	1886	----LSMDSPSD--LSPNAPPVGFENTAQFLEKLQQE-DRPSAEGSIDSSGFEKVDHE--	1936
Qy	563	MDLVQTSEVMQESLYPAAQLCPSEFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS	622
Db	1937	-----GLDEFAAPP-----VHDPMQSKSVFGLSGSDDMKPGS	1967
Qy	623	SP-----LEASSVNYESI KHEPE AMSVSLKVSGIKKEEIKEPENIN-----AAL	672
Db	1968	QDDGFVFIERNAN-----EATLKKNQKMSHHNDVIEKNYFNDNAPTAAL	2013
Qy	673	QETEAPYISIIACDLIKETKLSAEPAPDFS DYSEMA-----KVEQPVPDHSSEL	719
Db	2014	--LESPIAEEARKLVQDAVESA-----SEYKKQAVDSGDEIGRELLDNVEQKIEQVKEP	2065
Qy	720	VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE	779
Db	2066	IVDSL--HKAYDGVGDFVHETV PNAVD DVFREAQQLPESPVPEKIE-----TPE	2113

Qy 780 GGKPYLESFKLSLDNTKDTL--LPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQ 837
 Db 2114 -----PLVDIHDTVDKVHDEVNDFLRREPTP-PFETDDVAPLSDDKPQFGNQTP 2161
 Qy 838 IRETETFSDDSSPIEIIIDEFPTLISSKTSFSKILAREYTDLEVSHKSEIANAPDGAGSLPC 897
 Db 2162 EEDETTFDRKGPLTIPEEVEKAAAAQNNDLD---DFDPLVTSNTGAAFGAAGVAAAA-- 2215
 Qy 898 TELPHDLSLKNIQPKVEEKISFSDDFSKNKSATSQVLLLPDVSALGHTQAEIESIVKPK 957
 Db 2216 -----VESLTEEM-----FGH--QKFETVPRPP 2237
 Qy 958 VLEKEAEKKLPDTEKEDRSPSAIFSADLG-----KT-- 989
 Db 2238 T-----PPKDISDEDVKPSTV---NLGPSHHSHSPSPHHSILKHHGDAWIDFKTVP 2286
 Qy 990 -SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQI 1048
 Db 2287 PCVLDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVTSLLLALGAAAGFRVFKKVEA 2346
 Qy 1049 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA 1108
 Db 2347 QIKKTDSEHPFSEILAQDLTLQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFG 2406
 Qy 1109 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 1168
 Db 2407 LVLWSLTYYIASWFSGFTLAILGLLGVSVPKVYESNQEAIDPHLATISGHLKNVQNIIDE 2466
 Qy 1169 KIPGLK 1174
 Db 2467 KLPFLR 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
 2586/2

Query Match 8.8%; Score 519.5; DB 2; Length 2607;
 Best Local Similarity 20.4%; Pred. No. 1.8e-13;
 Matches 292; Conservative 175; Mismatches 474; Indels 491; Gaps 55;

Qy	1	MEDLDQSP	LVSSSDSP	PRPQPA	FKYQFV	REPEDEEE	-----EE	38		
Db	1397	LEKVEVQP	--DLSQ	NSPAPHKI	IDLHF-NI	PKDHEDY	GNDYVFP	FGTESSEESQKADGNQE	1453	
Qy	39	EEEEED	-----	EDEDLEE	LEVLER	KPA----	AGLSAAP	-----	67	
Db	1454	NQEEED	VVAELNF	HPIRQWR	DEDIVI	SLQSLK	SLVAE	VGCI TDVDASDVNEQDEESTLKIL	1513	
Qy	68	--VPTA	PAAGAP	LMDFGN	DFVPPA	PRGPLPA	APPVAP	--ERQPSW	-----	108
Db	1514	KVVPSE	PSLLE	--LDFT	ND--	PKVIHV	PIPLME	PATMYLEEMVEWIIADAVKEVSEMEVV	1569	
Qy	109	-----	DPSPVS	STVPAP	SPLSAA	AVSPSK	LP-EDDE	PPARPPPPPPASVSPQAEVW	159	
Db	1570	TESEIS	EMAPQV	SESTCP	IPPEL	-----	ADLKL	PVEDDEKTPEPEPVVPGQVQERIIPIE	1624	
Qy	160	TPPAPA	-PAAPP	STP----	AAPKRR	GSSGAV	VXXXXX	KIMDLKEQPGNTISAGQE---	208	
Db	1625	VEQAPT	IPQRPP	RAPKSEL	PKVAK	PLDDSKS	-----	RVRFAPLNKILGRTYSEEQQKEL	1678	
Qy	209	----	DFPSVL	LETAAS	XP-----	SLSPLS	AASFKE	HEY--LGNLSTVLPTEGTLQEN	254	
Db	1679	VESLER	PLTII	-TQQK	PPEKPT	EDIGALS	SPLSPN	TLAEEYEEVPMMDMQSVPHSPQEKQEE	1737	
Qy	255	VSEASKE	VSEKAK	TLLIDR	DLTEF	SELEYSE	MSSFSV	SPKAESAVIVANPREEIIIVK--	312	
Db	1738	I-EALSE	IIIEEP	QAM-----	KEVEK	PVESAE	PKDNES	LEAPEIINEPIRRVLVETK	1787	
Qy	313	-----	NKDEEEK	LVSNNI	LHXQQE	LPTALT	KLKVE	DEVVSSEKAKDSFNEKRVAVEA	364	
Db	1788	5X	IMGPGK	SLNEDN	DDDDDG	SECLDS	SIGDL	-----SERTIQRFN--TSIDD	1829	
Qy	365	P--MREE	YADFKP	FERVVE	VKDSKED	--SDMLA	AAGGKI	ESNLESKVDDKKCFADSLEQTNH	420	
Db	1830	PSIRRD	SFSSIS	SFGDRQ	KFRTAI	ENIRQD	LLFPQ	SSVSQYLRSSPNP--SQQLLVTNL	1886	
Qy	421	EKDSESS	NDDTSF	PSTPEGI	-----	KDRSGA	--YITCA	PFNPAATESIATNIF	466	
Db	1887	SMDSPS	---DLSP	NAPPVG	FENTAQ	FLEKLQ	QEDRPS	AEGSIDSSGFVKVDHEGLDEFAA	1943	
Qy	467	PLLEDPT	SEN----	XTDEKK	-----	IEEKKA	QIVTEK	NTSTKTSNPPFFVAAQDS	511	
Db	1944	PPVHDPM	QKSVFG	SLGSD	DMKPGS	QDDGFV	FIERNE	ANEATLKKNQKMSSHNDVIEKNY	2003	
Qy	512	ETDYVTT	DNLT	TKVTEE	VVANMPEGL	CESELNEV	-TGTKI	AYE----	TKMDv	566n
Db	2004	FNDNAPT	---AALLES	PIAEEA	RKL	VQDAVES	ASEYKK	QAVDSGDEIGRELLDNVEQKIE	2060	
Qy	567	QTSEVM	QESLYP	AAQLCPS	FEESEAT	PSPVLP	DIVMEAP	LSAVPSAGASVIQPSSSPLE	626	
Db	2061	QVKEPI	VDLSLH	KAYDGV	GDFVH	-ETV	PNAV-DDFV	REAE-----	2097	
Qy	627	ASSVNYE	SIKHEP	ENPPPY	EEAMSV	SLKVSGI	KKEIK	EPENINAALQETEAPYISIACDL	686	
Db	2098	-----	KQLPES	PVP-----	EKIETPE	-----	PLVDI	HDTV	2122	

Qy 687 IK-----ETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDV 741
 | : | | | : | : | : | :
 Db 2123 DKVHDEVNDNFLRREPTPPFE-----TDDVAPLSDDKPQFGNQ T---- 2160

Qy 742 PQKQDETVM LVKESLTETS FESMI EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLP 801
 : | | | | : | : | : | : | : | :
 Db 2161 -PEEDETTFDRKGPLT-----IP 2177

Qy 802 DEVSTLSKKEKIPLQMEELSTAVYSNDDL FISK EAQIRETETFS DSSPIEIID EFP TLI S 861
 : | | : | : | : | : | : | : | :
 Db 2178 EEV-----EKA AAAQNND-----LDDFDPLVT 2199

Qy 862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890
 | | : | : | : | : | : | : | :
 Db 2200 SNTGA AFGAAVGAAA VESLTEEEMFGHQKFETVPRPPTPKDISDEDVK-PSTVNLGPS 2258

Qy 891 GAGSLPCTELPHD-----LSLKNIQPKVEEKIS-----FSDDFS 924
 | | : | : | : | : | : | : | :
 Db 2259 HHHSH PSS--PHHSILKHHGDWIDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFFS 2316

Qy 925 KNGSATS KVL LL-----PPDV SALG----- 944
 | : : | : | : | : | : | : | :
 Db 2317 KSLPLLDNLLSLVVYLSISLIHVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNI 2376

Qy 945 --HTQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKK 1002
 : : | : | | | | : | : | : | : | : | :
 Db 2377 VLRVGLNVALVVGVA VSAHEAYKLTKS-----SGVLRKKEVL DVIYWRDAKK 2423

Qy 1003 TGVVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAY 1062
 : : | : | : | : : : | | | | : : | : | : | : | : | : | :
 Db 2424 SAIVLSLALLVLFVLAKYPLLT VVTYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEI 2483

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122
 | : : : | : : : | : : | : : : | : : : | : : | : : | : : | : :
 Db 2484 LAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGLVLSLTYIASWFS 2543

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLK 1174
 | | | | : : | | : | : | : : | : | : | : | :
 Db 2544 GFTLAILGLLG VFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:

Query Match 5.7%; Score 340.5; DB 2; Length 222;
Best Local Similarity 32.4%; Pred. No. 1.4e-07;
Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;

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RESULT 7
I38346
elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38346
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and
elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: I38346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position:      -2q31      ----

```

Qy	32	EDEEEEEEEEEDEDEDLEELE--VLERK---PAAGLSAAPV-----PTAPA	73
		: : : :	
Db	6176	EEEREAAAAEAENVTEYEVMEPEEYVVEEKLHIISKRVAAEPAEVTERQEKKIVLPKPIPA	6235
Qy	74	AGAPLMDFGNDFVPPAPRGPLPAAP-PVAPERQPSWDPSVSTVPAPSPLSAAAVSPSK	132
		: : : :	
Db	6236	K-----IEEPPPAKVPEAPKKIVPEKK-----VPAPVP-KKEKVPPPK	6272

Qy 133 LPEDDEPPA---RPPP-----PPPASVS-----PQAEPVWTPPAPAPAAPPS-TPAA 175
: || : : | : || | || : | || | : |
Db 6273 VPEEPKKPVPEKKVPPKVIKMEELPAKVTEKHMQITQEEKVLVAVTKKEAPPKARVPEE 6332

Qy 176 PKRRGSSGAVVXXXXKIMDLK----EQPGNTISAGQEDF---PSVLLETAASXPS-LSPL 227
||| : : || : : : : : : | : | : :
Db 6333 PKR-----AVPEEKVLKLPKREEEPKAKVTEFRKRVVKEEKVSIKAPKREPQPIKEV 6385

Qy 228 SAASFKEHEYLGNLSTVLPTEGTLQEN-VSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
: || | || : | || : : : | || | : |
Db 6386 TIMEEKERAY-----TLEEEAVSVQREEEYEEYE---EYDYKEFEFEYEPTTEE 6429

Qy 287 GSSFS-----VSPKAESAVIV--ANPREEI 309
: POTE ||| | : | :
Db 6430 YDQYEEYEEREYERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPAKVLKKAVPEEKV 6489

Qy 310 IV---KNKDEEEKLVSNILHXQQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAP 365
| | | : : : : : | | | : | | |
Db 6490 PVPIPKKLKPPPKVPEEPKKVFEEKIHISITK--REKEQVTEPAAKVPMKPKRVVAEEK 6547

Qy 366 MREEYADFKPFERVWEVKDSKEDSMDLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425
: : | || | : : | : : : : | : || : |
Db 6548 VVPVPRKEVAPPVVPVPEVPKELEPEEV----AFEEVVTHVE-EYLVEEEEEEYIHEEE-E 6600

Qy 426 SSNDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEE 485
: : | | : : | | : : | | : : || ||
Db 6601 FITEEEVVPVPIPVKVPE-----VPRKPVPEEKPPVVPVKKKEAPPKVPPEVPKKPEE 6652

Qy 486 KKAQIVTEKNTSTKTSNPPF-----VAAQDSETDYVTTDNL----- 521
| : : | Pp*950XA| :
Db 6653 KVPVLI PKKEKPPPAKVPEVPKKPVPEEKVPVPVPPKVEAPPKVPPEVPKKPVPEKKVPV 6712

Qy 522 -----TKVTEEVVANMPEGLTPDLVQACESELNEVTGTIAIYETKMDLVQTSEV 571
|| | : || | | : | : : | : | ||
Db 6713 PAPKKVEAPPKVPPEVPKKLIPEEKKPTVPVKKVEAPPPKVPKKREPVPVPVALPQEEEV 6772

Qy 572 M-QESLYPAAQLCPSFEESEATP----- 593
: : | : : | || | |
Db 6773 LFEEIIVPEEEVLP--EEEEVLPEEEVLPEEEVLPEEEIIPPEEEVPPEEEYVPEEE 6830

Qy 594 -----SPVLPDI VMEAPLNSAVPSAGASVIQ-----PSSSPLEASSVNYESI- 635
||| : : | : | : | : | : | : |
Db 6831 EFVPEEEVLPEVKPVVPAPVPEIKKKVTEKKVVI PKKEEAPPKVPPEVPKKVEEKRII 6890

Qy 836 --KHE-----PENPPPYEEAMSVy EI---KEPENIN 669
| | || || || || : : || |
Db 6891 LPKEEEVLPEVTEEPPEEPISEEEIPEEPPSIEEV-----EEVAPPRVPEVIK 6939

Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEP 729
| : | | : | | || : : | : : |
Db 6940 KAVPEAPTVP-----PKKVEAPP-----AKVSKKIPPEKVPVPVQKKEAPP 6980

Qy 730 VDLFSDDSIPDVPOKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK 789
: : || : | : || | | : || | :
Db 6981 A-----KVPEVPKKVPEKKVLV-----PKKEAVPPAKGR----- 7009

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Qy      790 LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSP 849
          | : | : : | | : : | : : | | : : | : : | : :
Db      7010 -----TVLEEKVSVAFRQEVVVKERLELEVVEAEVEE--IPEEEEFHEVEEYFEEGE 7059

Qy      850 IEIIDEFPTLISSKTDSPFSKLAREYTDLEV--SHKSEIANAPDGAGSLPCTELPHDLSLK 907
          : : | | | : : : : : : | | : : | : | : : | |
Db      7060 FHEVEEFIKLEQHRVEEEHRVEKVHRVIEVF EAEEVEVF EKP KAPPKGP-----EISEK 7113

Qy      908 NIQPK-----VEEKISFSDDFS KNGSATS KVL L LPPDV SAL 943
          | | | | | : : : : : : : : : :
Db      7114 IIPPKKPPTKVVP RKEPPAKVPEVPKKIVVEEKVRVPEE-----PRVPP----- 7157

Qy      944 GHTQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSP 978
          : : : : | | | | | : : : : :
Db      7158 ----TKVPEVLPPK--EVVPEKKVPVPPAKKPEAP 7 86

```

RESULT 8

T13564

microtubule-associated protein homolog - fruit fly (*Drosophila melanogaster*)

N;Alternate names: hypothetical protein EG:49E4.1

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13564

R;Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17689

A;Accession: T13564

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5327 <SPA>

A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1

C;Genetics:

A;Cross-references: FlyBase:FBgn0025392

A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1

A;Note: EG:49E4.1

C;Superfamily: *Drosophila* 576K microtubule-associated protein homolog

Query Match 5.5%; Score 325.5; DB 2; Length 5327;

Best Local Similarity 23.6%; Pred. No. 4.6e-05;

Matches 275; Conservative 151; Mismatches 520; Indels 219; Gaps 53;

```

Qy      28 VREPEDEEEEEEEEE---DEDEDLEELEVLERKPAAGLS-----AAPVPTAPAAG 75
          : : : | : | | : : | : : | : : | : : | : :
Db      1277 MEQVKDKEEHEQKIESGIITEKEAKKSASTPEEKETSDITSDDDELPAQLADPTTVPPKSA 1336

Qy      76 APLMDFGND FVPPA-----PRGPLPAAPPV-APERQPSWDPSPV SSVTPAPSPLSAA 126
          | | : | | : | | | | | : | | : | |
Db      1337 KDREDTGSIESPPTIEEAIEVEVQAKQEAQKVPAPAEAAIKTEKSPLASK-ETSRPESAT 1395

Qy      127 AVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPA-----APK 177
          : | | | | | : : : : : : : : : :
Db      1396 ----GSVKEDTEQTKSKKSPVPSRPESEAKDKKSPFASGEASRPESVAESVKDEAGKA 1451

Qy      178 RRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----DFPSVLLETAASXP-SLSPLSA 229
          | | | : | | | : | | | | | : : |

```

Db 1452 RRESIAKTHKDESSLDKAKEQESRRESIAESIKPESGIDEKSALASKEASRPESVTDKS- 1510
 Qy 230 ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSS 289
 || : : | | | : || | : : | | | : :
 Db 1511 ---KEPSRRESIAESLKAESTKDEKSAPPSKEASRPGSVVESVKDETEKSKEPSRRESIA 1567
 Qy 290 FSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSN---ILHXQQELPTALTCLVKEDEVV 346
 | | | : | | : || | | : : | : : | : :
 Db 1568 ESAKPPIEFRE-VSRP-ESVIDGIKDESAKPESRRDSPLASKEASRPESVLESVKDEPIK 1625
 Qy 347 SSEKAK-----DSFNEKRVAVE-APMREEYADFKPFERVWEVKDS--KEDSDMLAAGGKI 398
 | : || : : : || : : : : | | | : | | :
 Db 1626 STEKSRRRESVAESFKADSTKDEKSPLTSKDIS-RPESAVENVMDAPFKETSRPESAVGSM 1684
 Qy 399 ESNLESKVDDKKCFADSLQVTHPE7KDEZSSNDTSFP-STPEGIKDRSGAYIT(455
 : || : | : | || : : : || | | | || | |
 Db 1685 KDESMSK-----EPSRRESVKDGAAQSRETSRPASVAESAkd--GADDLKELSRP 1732
 Qy 456 AATE-----SIATNIFLLEDPTS-----ENXTD--EKKIEEKKAQIVTEKN--TSTK 499
 : | || || : | : | || || : : | || : :
 Db 1733 ESTTQSKEAGSIKDEKSPLASEEASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKE 1792
 Qy 500 TSNPFFVAAQDSETDYVTTDNLTkvTEEVVANMP----EGLTPDLVQEACESELNEVTGT 555
 | | || : | | | | | | | | : : |
 Db 1793 ASRPASVA--ESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDE----AE 1845
 Qy 556 KIAYETKMDLVQTSEVM--QESLYPAAQLCPSFEESEATPSPVLPDIVME-APLNSAVPS 612
 | | : : | : : || : : : : | | : || | |
 Db 1846 KSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEAS 1905
 Qy 613 SPLEASSVNYESIKHEPENPPPYEAMSSVSLKVSGIKEEI---KEPENIN 669
 ||| : | | : : | | : : || : | ||
 Db 1906 RPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRE 1965
 Qy 670 AALQETEAPYISIACDLIKETKLSAEPAPPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEP 729
 : : : | || | | | : : | | | : ||
 Db 1966 SVAEKSPLP-----SKEASRPASVAESIKDEAEKSKEE---SRRESVAEKSP---- 2009
 Qy 730 VDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIE--YENKEKLSALP-PEGGKP--Y 784
 : | : | || : : : : | | : : | | | : |
 Db 2010 -----LPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASV 2058
 Qy 785 LESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEE----LSTAVYSNDDLFIKSEAQIRE 840
 || | : : | : | | || || : | | | : || |
 Db 2059 AESIKDEAEKSK-----EESRRESAAEKSPLPSKEASRPASVAESVKDEADKSKEESRR- 2112
 Qy 841 TETFSDDSSPIEII--DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898
 | : : : | : | : : | : | | | : ||| :
 Db 2113 -ESMAESGKAQSIKGDQSPLKEVSRPES---VAESVKDDPVKSK-EPSRRESVAGSVTAD 2167
 Qy 899 ELPHDLSLKNIQPKVEEK-----ISFSDDFSKNGSATS KVL LPPDVSA LGHTQAE 949
 | : : | : | | | : | | : : :
 Db 2168 -----SARDDQSPLESKGASRPESVVD SVKDEAEKQES-----RRESK 2205
 Qy 950 IESIVKPKVLEKEAEKKL- ----PSDTEKEDR-SPSAIFSADLGKTSVVDLLYW---RDI 1000
 || : : | : : | : : || | | : : : : ||
 Db 2206 TESVIPP KAKDDKSPKEVLQPVSM TETIREDADQPMKPSQAESRRESIAESIKASSPRDE 2265

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Qy      1001 KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFR 1060
          |          | |          | : : | : : | | | | |
Db      2266 KSP-----LASKEASRPGSV-----AESIKYDLDPQIIKDDKSTE-HSRR 2305

Qy      1061 AYLESEVAI-SEELVQKYSNSALGH 1084
          | | : | : | | : : | |
Db      2306 ESLEDKSAVTSEKSVSRPLSVASDH 2330

```

RESULT 9

A47282

calcium-binding protein calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: A47282

R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993

A;Title: Calphotin: a *Drosophila* photoreceptor cell calcium-binding protein.

A;Reference number: A47282; MUID:93165729; PMID:8094559

A;Accession: A471;

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-865 <MAR>

A;Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032

A;Experimental source: photoreceptor cells

A;Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)

C;Genetics:

A;Gene: FlyBase:Cpn

A;Cross-references: FlyBase:FBgn0010218

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding

```

Query Match          5.5%; Score 324.5; DB 2; Length 865;
Best Local Similarity 22.3%; Pred. No. 4e-06;
Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

```

```

Qy      59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
          | : ||| | | ||: | ||| | : | | | : | | : |
Db      9 PVSAPVAAPV-TPSAVAAPVQVVSAPAAVAPAP APIAVTPVAPPPTLASVQPATV--TIP 65

Qy     119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAP---APAAPP--ST 172
          ||:|::||:|:| | | | |||: || : || | | || || : |
Db     66 APAPIAAASVTP---VASVAPPVVAAPTTPAA-SPVSTPVAVAQIPVAVSAPVAPPVAAT 121

Qy     173 PAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232
          | : : | : | | | | | : | | | : | | : | : |
Db     122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160

Qy     233 KEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292
          | : | | | | : : | : : | : : | : |
Db     161 -----PPVVPANTT----VPVAAPVAAPVAAPVVPVAPVLAP-----AV 194

Qy     293 SPKAESAVIVAN-----PREEIIVKKNDEEEKLVSNILHXQQELPTALTCLVKEDEVVS 347
          : | | : || | || | : | : | 2 || :
Db     195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVA 234

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Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407
 : | : | | | | | : : : : |
 Db 235 T---KPLAAAEPVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

Qy 408 KKCFAADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467
 || : : | : | || ||
 Db 281 -----ASTEPPV---AAATLTAPETPAL----- 301

Qy 468 LLEDPTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527
 | : | | || | | | |
 Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579
 | || : | : | : | || : | || : | || : ||
 Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371

Qy 580 -AQLCPSFEESEATPSPVLPDIOMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHE 638
 | | : : | : | || : : | : || : | : | :
 Db 372 PATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431

Qy 639 PENPPPYEEAMSV-SLKVSGIKKEIKPENINAALQETEAPYISIACDLIKETKLSAEP 697
 || | | : : : | : : | : | || : | : : | ||
 Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVSTPPTTASVPETTAPPA 491

Qy 698 P-----DFSDYSEMAKVEQVPDPHSEL-----VEDSSPDSEPVDLFSDDSI--DVPQK 744
 | | || | : | || : | | : | || : | : |
 Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDL 550

Qy 745 QDETVMLVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEV 804
 : : | : : | : : p : : || : : : : \$ 60
 Db 551 LEQTTSPVAEEAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603

Qy 805 STLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETFSOSSPIEIIIDEFPTLI 860
 | : | || : : : | || | : || | | | || :
 Db 604 SLATPTEPIPVEAPVVIQEAVDV-----EVPVTETST---SIP-ETTVEFPEAV 649

Qy 861 SSKTDSFSLKAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDLSSL 906
 : | | : | : : : || || | || : | : :
 Db 650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701

Qy 907 KNIQPKVEEKISFSDDFSKNGSATSQVLL---LP-----PDVSALG----- 944
 | | | : : : : : : : : : | : ||
 Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760

Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPDTEKE Q88NFSADLGKTSVVDLLY 996
 : | | : | | : || : : : : || | : | : ||
 Db 761 ITAGDNPDNSTVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814

Qy 997 WRDIKKTGV 1005
 || : | |
 Db 815 -RDLQTTDV 822

Qy 572 MQESLYPA-----AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS 622
 ||: || : : : : || : : : || : :
 Db 365 AAESI-PAPVVATTPVPATLAVTDPDVTASAVPELPPVIAAPSPVPSAVAETPVDLAPPVL 423

 Qy 623 SPLEASSVNYESIKHEPENPPPYEEAMSV-SLKVSGIKKEIKEPENINAALQETEAPYIS 681
 |: | : || | : : : : : | : | : |
 Db 424 PPVAAEPVPAVVAETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAAPIVS 483

 Qy 682 IACDLIKETKLSAEPAP-----DFSDYSEMAKVEQVPDPHSEL-----VEDSSPDSEPV 730
 : : | || | | | : | || : | : |
 Db 484 TPPTTASVPETTAPPAAVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAE 542

 Qy 731 DLFSDDSSIP--DVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788
 || : | : | : : : : : : : : ||
 Db 3 DLIIIEPVEPPAPIPDLLEQTTSVPAVEAAESTSSPIPE-----TSLTARNENALAPSEV 595

 Qy 789 KLSLDNTKDTLLPDEVSTLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETF 844
 : : : : | | : | || : : : | | : | ||
 Db 596 AVAPITAPEPIPEPEPSLATPTEPIVPEAPVVIQEAVDV-----EVPVTETST- 644

 Qy 845 SDSSPIEIIDFPTLISSKTD SFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-- 901
 | | | ||| : : | | : | : : : || ||| | ||:
 Db 645 --SIP-ETTVEFPEAVA EKV-----LDP AITEAPVTTQEPDVANINDGA---PATEITTP 693

 Qy 902 -----HDSLKNIQPKVEEKISFSDDFSKNGSATSKVLL---LP-----PDVS 941
 | : : | | | : : : : : : : : : : | : ||
 Db 694 AVEIVTAAAEVSDTAIPLIDPPVPQEIAVA-EIPETETKPAEVIVEQSTIPIEAPVPEVS 752

 Qy 942 ALG-----HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSA 980
 : | | : | | : | | : | : : ||
 Db 753 KYAEPVISEAPAAEVPITAGDNPDN TSVGISEVV-PTIAEKPV EEVPTSEIPEQSSSPSD 811

 Qy 981 IFSADLGKTSVVDLLYWRDIKKTGV 1005
 | : | : || || : : ||
 Db 812 --SVPVAK--ITPLL--RDLQTTDV 830

RESULT 11

T34418

hypothetical protein F12F3.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34418

R;Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of *C. elegans* cosmid F12F3.

A;Reference number: Z21521

A;Accession: T34418

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3488 <FUL>

A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3

A;Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: CESP:F12F3.3

A;Map position: 5

A; Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1

Query Match 5.1%; Score 299.5; DB 2; Length 3488;
Best Local Similarity 20.6%; Pred. No. 0.0003;
Matches 272; Conservative 187; Mismatches 475; Indels 387; Gaps 57;

```
Qy      1 MEDLDQSPLV--SSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEV--- 54
      ::::| | ::      | : :| | : ::| | | :      | | : : |::|
Db      340 VDEVDSTVLEEKDDGDDKSKPKTKKKIIKKKETPESEQVTAAEPEQQKISEVDVQSV 399

Qy      55 -----LERKPAA---GLSAAPVPT-----APAAGA-----PLMD-----FGNDF 85
      :|| | | || | :      | |      | |      | |
Db      400 ETEVGAKKKPDAEKPTDLSKAKKDSKSKKSDEPEASTEESTTEKPTNDKTSKKSAEKKT 459

Qy      86 VPPAPR---GPLPAAPPVAPERQPSWDPSPVSSTVPA-----PSPLSAAAV 128
      | |      || | || : : | |      | : ||      | : : :
Db      460 VKPKKEVTGKPLEAKKPVEDKKDASQPSSSKESSPPTDGKKKKQIPKALFIPDEISSRFG 519

Qy      129 SPSKL-----PEDDEPPARPP--PPPPASVS-----PQAEPVWTPPA
      || :      :      | : | | ||||      : || : :
Db      520 DPSTMHSETNITTTIRGREGSADAKTPLVEPLSASVSMKVFTLVESAKEKAEFSEFKRRSE 579
                                           164 50XE

Qy      165 AP-----AAPPSTPAAPK-----RRGSSGAVVXXXXKIMD----LKEQPGN----- 201
      |      || : : | : : | : | : : | : | : : || :
Db      580 TPDDKSRKKEGLPPAKKSEKKEVTAEKQSTEALIESKKKEVDESKISEQQPSDKNKSEV 639

Qy      202 ----TISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGNLSTVL---PTEGTLQEN 254
      : || | |      | : : | : : | : | | | : : : :
Db      640 VGVPEKAAGPETKKDV--SEIEEVPKKKTIKKKTEKSDSSISQKSNVLKPADDDKSKSDD 697

Qy      255 VSEASKEVSEKAKTLLID-----RDLTEFSELE-----YSEMGSSFSVSP 294
      | : | | : : | : | | : | | : : | : | | : |
Db      698 VTDKSKKTTEDQTKVATDSKLEKAADTTKQIETETVVDDKSKKKVLKKKTEKSDSF-ISQ 756

Qy      295 KAESAVIV--ANPRE----EII VKNKDDEEKLVSNNILHXQQELPTALTCLKVKED----- 343
      | : | : | | | : | | | : : | | : | : : | | : |
Db      757 KSETPPVVEPTKPAESEAQKIAEVNKAQKQKEVDDNL---KREA EVAAKKIADEKLKIEA 813

Qy      344 -----EVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 395
      || : : | | : : : : | : : | : : | : : | : |
Db      814 EANIKKTAEEVAACKQKEKDEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEAD---AVK 870

Qy      396 GKIESNLESKVD--KKCFAD--SLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCA 451
      : | | : : | : || || || : : | : | : | | | : : |
Db      871 KQKELNEKNKLEAAKSAADKLKLEEESAASKVKVSEESVKF---GEEKKTKAGEKTVQV 927

G      Qy      452 PFNPAATESIATNIFPLL      SENXTDEKKIEEKKAQIVTEKN$B$DKTSNPFVAAQDS 511
      | : : : | | | | | : ||| : || ||| : | : : | |
Db      928 ESEPTSKKTIDTKDVGATE-PADE--TPKKKIIKKK---TEKSDSS-----ISQKS 972

Qy      512 ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGK-----IAYETKMDL 565
      || : : : | | : | : | | | : : | : | | | : | :
Db      973 ATD---SEKVSQKEQDEPTKPAVSETQMVTEADKSKKQKETDEKLKLD AEIAAKTKQEA 1029

Qy      566 VQTSEV-MQESLYPAAQLCPSFEESEATPSPVLPD-IVMEAPLNSAVPSAGASVIQPSSS 623
      : | : : | | : : | : | | | : : | : : | | : :
Db      1030 DEKSKLDAQEKIKKVS-----EDDAARKEKELNDKLKLESEIATKKASADKLKLEEQAQ 1083
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A;Residues: 1-3924 <CHA>
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
 R;Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins
 reveal a family of alternatively spliced genes.
 A;Reference number: A39643; MUID:91302466; PMID:1830053
 A;Accession: A39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2077 <OT1>
 A;Cross-references: GB:X56957
 A;Accession: B39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1443,3585-3924 <OTT>
 A;Cross-references: EMBL:X56958
 R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux,
 S.E.; Ward, D.C.; Forget, B.G.
 Genomics 10, 858-866, 1991
 A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin
 gene.
 A;Reference number: A40334; MUID:92009921; PMID:1833308
 A;Accession: A40334
 A;Molecule type: DNA
 A;Residues: 463-474, 'PE', 477-495 <TSE>
 A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
 R;Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A;Title: 440-kD ankyrinB: structure of the major developmentally regulated
 domain and selective localization in unmyelinated axons.
 A;Reference number: A49462; MUID:94075409; PMID:8253844
 A;Accession: A49462
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-3924 <RES>
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
 C;Genetics:
 A;Gene: GDB:ANK2
 A;Cross-references: GDB:127607; OMIM:106410
 A;Map position: 4q25-4q27
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing
 F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
 F;2-11 -3924/Product: ankyrin 2, short form #status predicted <MA2on50Xm
 F;63-95/Domain: ankyrin repeat homology <AN01>
 F;96-128/Domain: ankyrin repeat homology <AN02>
 F;129-161/Domain: ankyrin repeat homology <AN03>
 F;162-190/Domain: ankyrin repeat homology <AN04>
 F;191-223/Domain: ankyrin repeat homology <AN05>
 F;232-264/Domain: ankyrin repeat homology <AN06>
 F;265-297/Domain: ankyrin repeat homology <AN07>
 F;298-330/Domain: ankyrin repeat homology <AN08>
 F;331-363/Domain: ankyrin repeat homology <AN09>
 F;364-396/Domain: ankyrin repeat homology <AN10>
 F;397-429/Domain: ankyrin repeat homology <AN11>
 F;430-462/Domain: ankyrin repeat homology <AN12>

F;463-495/Domain: ankyrin repeat homology <AN13>
 F;496-528/Domain: ankyrin repeat homology <AN14>
 F;529-561/Domain: ankyrin repeat homology <AN15>
 F;562-594/Domain: ankyrin repeat homology <AN16>
 F;595-627/Domain: ankyrin repeat homology <AN17>
 F;628-660/Domain: ankyrin repeat homology <AN18>
 F;661-693/Domain: ankyrin repeat homology <AN19>
 F;694-726/Domain: ankyrin repeat homology <AN20>
 F;727-759/Domain: ankyrin repeat homology <AN21>
 F;760-792/Domain: ankyrin repeat homology <AN22>
 F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match 5.0%; Score 299; DB 2; Length 3924;
 Best Local Similarity 21.5%; Pred. No. 0.00037;
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

Qy 14 DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK 58
 | | : | : : : : | : | | |
 Db 1648 DIPDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAEKKGSSEESLGED 1707

Qy 59 PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----- 92
 | | : | : | : | : | : | : |
 Db 1708 P--GLAPEPLPTVKAT-SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKKGEDV 1764

Qy 93 -----PLPAA-PPVAPERQPSWDSP-----VSSTVPAPSPL 123
 | | | | : | | | | | | | |
 Db 1765 PKKTTHRPHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV 1824

Qy 124 SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW 159
 | : | | | | | : | | | : : | |
 Db 1825 SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSKTERHPPVSPSGKTDKRPV- 1883

Qy 160 TPPAPAPAAPPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLE 216
 : | | : | : : | | | | : | : : |
 Db 1884 SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLVPVSPSG 1934

Qy 217 TAASXPSSLPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT 268
 | : | | : | : | : | : | : | | |
 Db 1935 KTEKQPPVSPTSSTERIEETMSVRELMKAFQSGQDPSKHKTGLFEHKSAKQKQPEKGV 1994

Qy 269 -----LLIDRDLTEFSELEYSEMSSFSVSPKAES--AVIVANPREEIIIVKNKDE-- 316
 : | : : : | : | : | | | : | : |
 Db 1995 RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAEKRGVVRVSS----IGVKKEDAAG 2049

Qy 317 -EEKLVSNNI-----LHXQQELPTALTKLVKE-----DEVV 346
 : | : : | : | : | : | : | : |
 Db 2050 GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGMDLQISPDRKTSTDFSEVI 2107

Qy 7 SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVVEVKDSKED-----+0--- 388
 | : | : : | : : | | : : | :
 Db 2108 KQELEDNDKYQQFRLSEETEKALHLDQVLTSPFNTTFPLDYMKDEFLPALSLQSGALDG 2167

Qy 389 -SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDESSNDDTSFPSTPEGIKDRS 444
 | : | | : : | | | : | : | : : :
 Db 2168 SSESLEKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSLF--SPKKSEEQT 2225

Qy 445 GAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKAQIVTEKNTSTKTSNPF 504

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      |      :      | |      | ||:: |      ||: | : : |||::
Db      2226 G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTVEDSETSTESFQKE 2277

Qy      505 FVAAQDSETDYVTTDNLTkvTEEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKM 563
      : |      | : |      : | | | |      : ||      | : | : |
Db      2278 ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT----EAAACDEGQRTFGSS-AHKT-- 2330

Qy      564 DLVQTSEVMQESLYPAAQLCPSEFESEATPSPVL-----PDIVMEAP--LNSAV 610
      ||      ||      : : ||: | | |      | | : : | | | :
Db      2331 ---QTDSEAQES-----TATSDETKALPLPEASVKTDGTGSKPQGVRISPGGLELAL 2380

Qy      611 PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVSG 657
      || : | :      | | | | | : : | : | : | : | : | : |
Db      2381 PSRDSEVLSAVADDSLAVSHKDSLEASPVLEDNSSHKTPTSLEPSPLKESPCRDSLESSP 2440

Qy      658 IKEEIKE---PEN--INAALQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710
      : : : |      | : : | | : : | |      | : | : :      | | | : | : |
Db      2441 VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE 2490

Qy      711 QPVPDHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI 765
      |      : | : | |      | | | :      : | : |      : : | | |
Db      2491 Q-----TSLMESSGKSPLSPDTPSSEEVSYEVTPKTTDVSTPKPAVIHECAEED----- 2539

Qy      766 EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKK---EKIPLQMEELS 821
      : | | | |      | |      | | | :      | | : | | : : | : | | | |
Db      2540 DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEES 2589

Qy      822 TAVYSNDDLFI SKEA-QIRETETFSDDSPIEI IDEFPTLISSKTD SFSKLAREYTDLEVS 880
      : : | : |      | : : : | : | | |      | | : | : : | : | :
Db      2590 S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSES----- 2633

Qy      881 HKSEIANAPDGAGS-----LPCTELPHDLSLKN-----IQPKVEEKISF--SDD 922
      : | : |      | | |      | : | | : :      | | | : : | : : |
Db      2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPLPSSMDSNSSPEEVQFQPVVSKQYTFKM NED 2692

Qy      923 FSKNGSATSKVLLLPPDV SALGHTQAEIESIVKPKVLEKEAEKKLPSD-----TEKEDRS 977
      : : : :      : : : | | | |      | | | | |
Db      2693 TQEEPGKSEE-----EKDSESH LAEDRHAVSTEAEDRS 2725

```

RESULT 13

T16251

hypothetical protein F35A5.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

C;Accession: T16251

R;Leimbach, D.

submitted to the EMBL Data Library, January 1996

A;Description: The sequence of *C. elegans* cosmid F35A5.

A;Reference number: Z18485

A;Accession: T16251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1274 <LEI>

A;Cross-references: EMBL:U46675; NID:g1166613; PID:g1166621; PIDN:AAB52641.1;

GSPDB:GN00028; CESP:F35A5.1

A;Experimental source: strain Bristol N2; clone F35A5

C;Genetics:

A;Gene: CESP:F35A5.1

A;Map position: X

A;Introns: 1272/2

Query Match 4.9%; Score 290.5; DB 2; Length 1274;

Best Local Similarity 20.5%; Pred. No. 0.00017;

Matches 221; Conservative 126; Mismatches 417; Indels 313; Gaps 45;

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Qy      13 SDSPPRP--QPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPT 70
      | :|| | || :| | |||| | | : || :|| : ||
Db      2 SRAPPTPIKNPAKKWKPPWESVDEEEEME-----VDEETPAPSKLEKKPSLKRKDAPTKP 56

Qy      71 APAAGAPLMDFGNDVFPAPRGPPLAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSP 130
      | : || | | | | | | : | | | : || |
Db     57 VPSPGAP-----SPVPIKNPVKKWKAPWEDDEPMEEAPAAP-----VP 94

Qy     131 SKLPEDDEP---PARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVX 187
      :| | | | || : | : | | | | | :
Db     95 AKKVRDPSPKKVPAPKPRDASPKKIMAAKK---EPETLPAVPP-TPVKNPVKKFKAPWED 149

Qy     188 XXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP-SLSPLSAASFKEHEYLGNLSTVLP 246
      : | : | | | : | : || : | | | || : : |
Db    150 DEVDVEDVKDAP--TVPAKKTVPVLKKKEPAAAKPRDPSPKKAAPSKEHDPI-----VPP 202

Qy     247 TEGTLQENVSEASKEVSEKAKTLLIDRDL--TEFSELE-----YSEMGSFSVSPKA 296
      | | | | | : : | | : | | | : | | | :
Db    203 T-----PIKNPAKKWKPPWEDDEVPTTEEIKEPEPATRKVPALKKKKEPSTSVKPVVS 252

Qy     297 ESAVIVANPREEIIVKNKDE-----EEKLVSNNILHXQQELPTALTKL 339
      : : | : : || : | | : : : : | :
Db    253 D-----PSPTKKVPVKKEPEVPPTPIKNPTKKWKPPWEDETPVEEV--KEPPVPEKKAPV 305

Qy     340 VKEDEVVSSEKAKDSFNEKR-----VAVEAPMREEYADFKPFERVWEVKDSKEDS 389
      : | : : | || | | | | : : | | | | :
Db    306 LKKKDPAPAAKARDPSPSKAAPKKVEPSSPVVPTPVKNPVKKYKP---PWEVDDEPAE- 361

Qy     390 DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYIT 449
      | | | : || | : | | : : | | : | :
Db    362 -----EVKKPSAPEKK--TPVLKRKEPEPSSTTPSSDPSPKKAAPAVKPRDSSPKK 410

Qy     450 CAPF--NPAATESIATNIFPLLEDPTSE-----NXTDEKKIEE-KKAQIVTEKNTSTKTS 501
      | : | | | : : | : | | : || | : : |
Db    411 ATPLQADPKAQEVPPTPV----KNPVKKYKPPWEVDDEDPVEEVKQPEAPAKKTPVLKRK 466

Qy     502 NPFFVAAQDSETDYVTTDNLTKVTEEVVANMPE-----GLTPDLVQ---- 542
      | || : | | | | | || | |
Db    467 EP---AAKD-----TAKPATSKTPET---PEKKDPVKPRDSSPKKVAAPKPSAQAPAT 513

Qy     543 -----EACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEES 589
      | | : : | : | : : || | | :
Db    514 PVKNPVKKWRPPWEDDETADDVSKPTDAKKTPSLAKKDPAPAKESLKPADTKAPAKPR 573

Qy     590 EATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAM 649
      : : | | | | : | | | | : | : | :
Db    574 DPSPKKVAP-----TAPEKKTVPVLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVP 623
```

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Qy      650 S-----VSLKVSGIK--EEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD 702
      :      :      : : | | | : : :      : | :      : | |
Db      624 AKPVPKTEVAPAAVKKPEPISKPKDTAPKKAEPNSPVV-----PPTP----- 665

Qy      703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFE 762
      | : | |      | |      : : | | |      | : : : | : | | : | |
Db      666 -----VKNPVKWKWKPPWEDDDAPAKPVSL-----PEPEKKTPVLAKKAPTKPDSE 710

Qy      763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822
      : | | |
Db      711 -----AAADPVSGP----- 719

Qy      823 AVYSNDDLFISKEAQIRETETFSDDSPIEII-----DEFPTLISSKTD SFSKLAREYT 875
      | : | : : | : : : | | : : : | : : |
Db      720 ---SSKDPKLAKKAPVKP----RDPSPMKAVPIKPAPKTEVPPAVVKKPEPVAK----- 766

Qy      876 DLEVSHKSEIANAPDGAGSLPCTELPHDL SLKNIQPKVE-----EKISFSDDFS KN GSA 929
      : | | | : : : | : : | : : | : : : |
Db      767 SRDPSPKK--AKAEPNSPVVPPT--PVKNPVKKWKPPWEDDDAPAEPVNVPEPEKKTPVL 822

Qy      930 TSKVLLLPPDVS'-----ALGHTQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSP 978
      | : | | | | | : : | : : | | | : | | |
Db      823 AKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKE---PSPKKAEPNSP 876

```

RESULT 14

A56577

microtubule-associated protein MAP 1B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997

C;Accession: A56577

R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.

Eur. J. Cell Biol. 57, 66-74, 1992

A;Title: Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.

A;Reference number: A56577; MUID:92347374; PMID:1639092

A;Accession: A56577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2364 <ZAU>

A;Cross-references: GB:X60550

A;Experimental source: brain

A;Note: nucleotide sequence not given; conceptual translation not complete

C;Superfamily: microtubule-associated protein MAP1B

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Query Match          4.9%;  Score 289;  DB 2;  Length 2364;
Best Local Similarity 20.9%;  Pred. No. 0.00047;
Matches 275;  Conservative 158;  Mismatches 462;  Indels 422;  Gaps 61;

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Qy      30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPA 89
      | | | | | | | : : | | : : | | | | : | |
Db      909 EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEDQY--DFL--- 963

Qy      90 PRGSESAAPP--VAPEEPPSWDPSVPSSTVPAPSPLSAAAVSPSKLPEDDEPPARPP *p975X9
      | | | : | : : | | : | | | | : | |
Db      964 ---GTPAKQPGVQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF 1011

```

Qy	148	PASVSPQAEFPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ	207
Db	1012	TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNREETESPSQ	1055
Qy	208	E-----DFPSVLLETAASXP---SLSPLSAASFKE----HEYLGNLSTVLPTEGTLQENV	255
Db	1056	EFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDTATDGRDYNASASTISPPSSMEEDKF	1115
Qy	256	SEAS-----KEVSEK-----AKTLLIDRDLTE	277
Db	1116	SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERSV-N	1174
Qy	278	FS----ELEYSEMSSFS-VSPKAESAVI---VANPRE---EIIVKNK-----	314
Db	1175	FSLTPNEIKASAEGEATAVVSFGVTQAVVEHCASPEEKTLEVVSQSVTGSAGHTPY	1234
Qy	315	----DEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSE--KAKDSFNEKRVAVEAPMRE	368
Db	1235	QSPTDEKSSHLPTTEVTENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE	1279
Qy	369	EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDDKKCFADSL	415
Db	1280	PVPDESSEPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSD--	1337
Qy	416	EQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNP--AATESIATNIFPLLED-	471
Db	1338	-----KESPVS-DLTSPLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE	1390
Qy	472	-----PTSENXTDEKKIEEKKAIIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTK	523
Db	1391	RKLGGDGSPTQVDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGAEDT--YSHMEGVAS	1447
Qy	524	VTEEVVA--NMPEGLTPDLVQEACESELNEVTGKIAIYETKMDLVQTSEVMQES-LYPAA	580
Db	1448	VSTASVATSSFPPTDD-VSPSLHAEVGSPhSTEVDDSLSVSVVQTPTTFQETEMSPSK	1506
Qy	581	QLCP-----SFESEATPSPVLPDI VMEAPLNSAV-----P	611
Db	1507	EECPRMSISPPDFSPKTAKSRTVPQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHP	1566
Qy	612	SAGASVIQ-----PSSSPLEASSVNYESI KHE--PENPPPY-----EEAMSVS-LKVS	657
Db	1567	TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEPSYTQDNDLSELISVSQVEASP	1626
Qy	658	IKEEIKEPENINAALQETE-----APYISACDLIKE---TKLSAEP-----	696
Db	1627	STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVSLEGEKLSPKSDISPLTPR	1686
Qy	697	-----APDFSDYSEMAK-----VEQPVPDHSELVEDS-----	723
Db	1687	ESSPTYSPGFSDSTSGAKESTAAYQTSSSPIDAAAAEPYGRSSMLFDTMQHHLALSRD	1746
Qy	724	-----SPDSEPVDLFSDD---SIPDVP---QKQD	746
Db	1747	LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYYEKTE	1806
Qy	747	ETVML-----VKESLTETSFSMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD	797

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      | :      | | : | :      | | : | | | |      : :
Db      1807 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTRTPEEGGYSY-----EISEK 1858

Qy      798 TLLPDEV--TLSKKEKIPLQMEELSTAVYSNDD-----LFISKEA 836
      | | | | | | | : : : | : | :
Db      1859 TTRTPEVSGYTYEKTERRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 1918

Qy      837 QIRETETFSDDSP-----IEIIDEFPTLISSKTD SFSKLAREYT-----DL 877
      | | | : | | | : : : : | | : | | | |
Db      1919 YSYETTTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 1978

Qy      878 -----EVSH-KSEIANA---PDG----AGSLPCTELPHDLSLKNIQP-----KV 913
      | | | : : : : | : | | | | : | :
Db      1979 CLVSSCEFKHPKTELSPSFINPNLEWFAGEEPTESERPLTQSGGAPPPSGGKQKQKQC 2

Qy      914 EEKISFSDDFSKNGSATS KSVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970
      : | | | | | | | | : | | | : | : : |
Db      2039 DETPPTSVSESAPSQTDSV---PPETE-----ECPSITADANLDSEDESETIPTDKT 2088

Qy      971 -----TEKEDRSPS-----AIFSADLGKTSVVDLLYWRDIKKTG 1004
      : | | | | | : | | | | | |
Db      2089 VTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAI EQNLGKALKKDLKEKAKTKKPG 2145

```

RESULT 15

QRMSP1

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663, 'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694,695-698,699-702,708-711,712-715,716-719,720-723,727-730,758-761,764-767,783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted
 F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted
 F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 289; DB 1; Length 2464;
 Best Local Similarity 19.8%; Pred. No. 0.0005;
 Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;

```

Qy      32 EDEEEEEEEEEDEDEDL-EELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAP 90
      | | : | | | | | | : | | : | | : | | : |
Db      1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVMAVADKAAEAGVTEEQYGY----- 1061

Qy      91 RGPLPAAPPV-APERQPSWDPSVSPSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA 149
      | : : | | : | : | | : | | : | | : | |
Db      1062 LGTSAKQPGIQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTA 1112

Qy     150 SVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209
      : : : | | | | : | : | | |
Db     1113 TSGYTQSTIEISSEPTPMDEMSTP-----RDVMSDETNNETESPSQEF 1156

Qy     210 FPSVLLETAASXPSLSPLSAAFSK-----EHEYLGNLSTVLPTEGTLQENVSE 257
      | : : | : | | : | : | | : | : |
Db     1157 VNITKYESSLYSQEYSKPAVASFNGLSEGSKTDATDGKDYNASASTISPPSSMEEDKFSK 1216

Qy     258 AS-----KEVSEK-----AKTLLIDRDLTEFS 279
      : : | : | : | : | : | : |
Db     1217 SALRDAYCSEEEKELKASAELDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERSV-NFS 1275

Qy     280 ---ELEYSEMSSFSVSPKAESA VI---VANPRE---EII VKNK----- 314
      | : | | : | | | | : | | : :
Db     1276 LTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTPPYYQSP 1335

Qy     315 -DEEEKLVSNNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF 373
      | | : : : | : : : | | | | : | |
Db     1336 TDEKSSHLPTVESENAQAVPVSF-----EFSEAKDE-NER--ASLSPMDEPV PDS 1382

Qy     374 K-PFERVWE-----VKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE 425
      : | | : : : | : | | : |
Db     1383 ESPVEKVLSPLRSPPLLGSESPYEDFLSADSKVLGR-----RSESPFE 1425

Qy     426 SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXT----- 478
      | | : : | : | : | : | | : |
Db     1426 GKNGKQGFPDRESPVSD-----LTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS 1480

Qy     479 -----DEKKI-----EEKKAQIVTEKNTSTKTSNPFVAAQDSETD 514
      | | : : : : | : | : | : |
Db     1481 SQSALALDERKLGGDVSPQTQIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDT 1538

Qy     515 YVITDNLTKVTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVM 572
      | : : | : | | | | : : | : : : |
Db     1539 YSHMEGVASVSTASVATSSFPPTTDD-VSPSLHAEVGSHPSTEVDDSLSVSVVQTPTTF 1597

Qy     573 QES-LYPAAQLCP-----SFEESEATPSPVLPDIVMEAPLNSAV-- 610
      | : : | : | : : : : | : :
Db     1598 QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD 1657

```

Qy 611 -----PSAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAM 649
 | : |||| : | : | : | : | :
 Db 1658 FSRQSPDHPTLGASVLHITENGPTVDYSPCDIQDSSLSHKIPPTTEPSYTDNDLSELI 1717

Qy 650 SVS-LKVSGIKEEIKEPENINAALQETE-----APYISIACDLIKE---TKLSAE 695
 ||| : : | | : ||| : | : | : : : ||| :
 Db 1718 SVSQVEASPSTSSAHTPSQIASPLQEDTLDVVPREMSLYASLASEKVQSLEGEKLSPK 1777

Qy 696 P-----APDFSDYSEMAK-----VEQPVPDHSELVEDS- 723
 : | ||| : || : | | : : | :
 Db 1778 SDISPLTPRESSPLYSPGFSDDSTSAAKETAAAHQASSSPPIDAATAEPYGRSSMLFDTM 1837

Qy 724 -----SPDSEPVDLFSD-----DS 737
 ||| | | | |
 Db 1838 QHHLALNRDLTTSSVEKDSSGKTPGDFNYAYQKPENAAGSPDEEDYDYESQEKTIIRTHDV 1897

Qy 738 IPDVPQKQDETVML-----VKESLTETSFESMIEYENKEKLSALPPEGKPYLESF 788
 : : | : | : | : | : | : | : | :
 Db 1898 VRYYYEKTERTIKSPCDSGYSYETIEKTTKTPEDGGYTCEITEKTTTRTPEEGGYSY---- 1953

Qy 789 KLSLDNTKDTLLPDEVSS--TLSSKEKIPLQMEELSTAVYSNDD----- 829
 : : : | ||| | | : : : : | :
 Db 1954 ----EISEKTTRTPEVSGYTYEKTERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEK 2009

Qy 830 --LFISKEAQIRETETFSDDSP-----IEIIDEFPTLISSKTDSFSLAREYT----- 875
 | | : ||| : || | : : : | : | :
 Db 2010 ITSFPESSESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTTTEKKSP 2069

Qy 876 -----DL-----EVSH-KSEIANA---PDG---AGSLPCTELPHDLSLKNIQP--- 911
 || | | : : : : | : || | | : |
 Db 2070 SEARQDVDLCLVSSCEFKHPKTELSPSFINPNLEWFAGEEPTEESEKPLTQSGGAPPPS 2129

Qy 912 -----KVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAE 964
 : : | | | | | || : | || : : | |
 Db 2130 GKGQQRQCDETPPTSVSESAPSQTDSDV---PPETE-----ECPSITADANIDSEDE 2179

Qy 965 KK-LPSD-----TEKEDRSPS-----AIFSADLGKTSVVDLLYWR 998
 : : | : | : |||| : ||| ||
 Db 2180 SETIPTDKTVTYKHMDPPAPMQDRSPSPRHPDVSMVDPDALAVDQNLGKAVKKDLKEKT 2239

Qy 999 DIKKTG 1004
 |||
 Db 2240 KTKKPG 2245

Search completed: January 22, 2004, 16:32:56
 Job time : 45.1516 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 61.624 Seconds
(without alignments)
4932.919 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	4851	81.9	986	4	Q8IUA4	Q8iua4 homo sapien
2	4289	72.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
3	4277.5	72.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
4	3658.5	61.8	1046	11	Q8BGK7	Q8bgk7 mus musculu
5	2527	42.7	639	11	Q8K290	Q8k290 mus musculu
6	1531	25.8	392	4	Q96B16	Q96b16 homo sapien
7	1201.5	20.3	375	11	Q8BHF5	Q8bhf5 mus musculu
8	1163	19.6	356	11	Q8BH78	Q8bh78 mus musculu
9	1152.5	19.5	357	11	Q8K3G7	Q8k3g7 mus musculu
10	867	14.6	179	6	Q9GM33	Q9gm33 macaca fasc
11	788.5	13.3	760	13	Q90638	Q90638 gallus gall
12	779	13.2	780	11	Q8K4S4	Q8k4s4 mus musculu
13	778	13.1	780	11	Q8K0T0	Q8k0t0 mus musculu
14	699	11.8	643	11	Q8CCU2	Q8ccu2 mus musculu
15	688	11.6	199	4	Q9BQ59	Q9bq59 homo sapien
16	672	11.3	208	13	Q90637	Q90637 gallus gall
17	671	11.3	267	11	Q63765	Q63765 rattus sp.
18	626	10.6	237	11	Q8C6D5	Q8c6d5 mus musculu
19	623.5	10.5	236	11	Q8VBU0	Q8vbu0 rattus norv
20	566	9.6	595	5	Q9VMV9	Q9vmv9 drosophila
21	528	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
22	528	8.9	2484	5	Q9U347	Q9u347 caenorhabdi
23	526	8.9	224	5	Q9VMW1	Q9vmw1 drosophila
24	520	8.8	222	5	Q9VMW4	Q9vmw4 drosophila
25	519.5	8.8	2607	5	Q23187	Q23187 caenorhabdi
26	518	8.7	202	5	Q9VMW2	Q9vmw2 drosophila
27	357.5	6.0	2768	5	Q9VC00	Q9vc00 drosophila
28	341.5	5.8	5412	5	Q9W596	Q9w596 drosophila
29	340.5	5.7	222	5	Q23188	Q23188 caenorhabdi
30	339	5.7	1150	5	Q8IMM6	Q8imm6 drosophila
31	334	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
32	334	5.6	18074	5	Q9I7U4	Q9i7u4 drosophila
33	331	5.6	7962	4	Q10465	Q10465 homo sapien
34	331	5.6	34350	4	Q8WZ42	Q8wz42 homo sapien
35	325.5	5.5	5327	5	O76891	O76891 drosophila
36	322.5	5.4	846	5	Q8MRP6	Q8mrp6 drosophila
37	322.5	5.4	1109	5	Q9VAY4	Q9vay4 drosophila
38	318	5.4	864	5	Q9VGC8	Q9vgc8 drosophila
39	317.5	5.4	4969	11	Q8CF91	Q8cf91 mus musculu
40	317.5	5.4	5165	11	Q8CF92	Q8cf92 mus musculu
41	316	5.3	842	5	Q9VGC9	Q9vgc9 drosophila
42	315	5.3	10578	5	Q8ISF5	Q8isf5 caenorhabdi
43	315	5.3	18519	5	Q8ISF6	Q8isf6 caenorhabdi
44	315	5.3	18534	5	Q8ISF7	Q8isf7 caenorhabdi
45	314	5.3	864	5	Q95U45	Q95u45 drosophila

ALIGNMENTS

RESULT 1

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.
AC Q8IUA4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Qy 433 FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDEKKIEEKKAQIVT 492
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 241 FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIVT 300

Qy 493 EKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV 552
 ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
 Db 301 EKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV 360

Qy 553 TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPS 612
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 361 TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPS 420

Qy 613 AGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL-KVSGIKEEIKEPENINAA 671
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 421 AGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAA 480

Qy 672 LQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVEQVPDPHSELVEDSSPDSEPVD 731
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 481 LQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVEQVPDPHSELVEDSSPDSEPVD 540

Qy 732 LFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS 791
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 541 LFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS 600

Qy 792 LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIE 851
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 601 LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIE 660

Qy 852 IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP 911
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 661 IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP 720

Qy 912 KVEEKISFSDDFS KNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDT 971
 ||||||||||||||||||||||||||||| ||||||||||||| |||||||||
 Db 721 KVEEKISFSDDFS KNGSATSKVLLLPDVSALA-TQAEIESIVKPKVLVKEAEKKLPSDT 779

Qy 972 EKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL 1031
 ||||||||||||| : |||||||||||||||||||||||||||||
 Db 780 EKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL 839

Qy 1032 ALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE 1091
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 840 ALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE 899

Qy 1092 LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY 1151
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 900 LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY 959

Qy 1152 LGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||||||||||||||||||||||
 Db 960 LGLANKNVKDAMAKIQAKIPGLKRKAE 986

RESULT 2

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.
 AC Q8BGM9;

Db 224 PLSTVSFKEHGYLGNL SAVASTE GTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE 283
 Qy 286 MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEV 345
 |||||: ||| |||:| | :||:| |:|: || : || || | |||:|||| |
 Db 284 MGSSFNKSPKGESAMLVENTKEEVI VRSKDKED-LVCSAALHNPQESPATLTQVVKEDGV 342
 Qy 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404
 :| || | ||| :| ||:||||||| |: ||||: | | |:||| :|:|
 Db 343 MSPEKTMDFNEMKMSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA---RANMES 398
 Qy 405 KVDKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN 464
 ||||| |||| | |||| |: || ||| :|| | |||| | |: :||| | |
 Db 399 KVDKKCFEDSLEQKGHGKDESRNENASFPRTPELVKDGSRAYITCDSFS-SATESTAAN 457
 Qy 465 IFPLLEDPTSENXTDEKKIEBKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKV 524
 |||:||| |||| | |||| |: ||| || | |||| | || | ||||| |:|
 Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVLVAIHDSEADYVTTDNLSKV 516
 Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGKTIAYETKMDLVQTSEVMQESLYPAAQLCP 584
 || ||| ||||| ||||| ||||| ||||| |: ||||| :|||:| |||||
 Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGKTIAYETKVDLVQTSEAIQESIYPTAQLCP 576
 Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPP 643
 ||||:||||||| ||||| :|| |||| |||:|||| | |:|: || |||||
 Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQSPASPLEVPSVPVSYDGIKLEPENPP 636
 Qy 644 PYEEAMSVSLKVGSIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDY 703
 ||||| |:| | ||||| |: ||| || ||||| ||||| |:|:| |
 Db 637 PYEEAMSVALKTSDSKEEIKEPESFNAAQEAEPYISIACDLIKETKLSTEPSPEFSNY 696
 Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFS 763
 |:| | |: |||| |:| |:| |:| |:| |:| |:| |:| |:| |:|
 Db 697 SEIAKFEKSVDPDHCELVDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVS-ET 755
 Qy 764 MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823
 : :|:| |:| | | ||||| |:| ||| :|: |:| | | |||| |:|
 Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTCKETISLQMEEFNTA 814
 Qy 824 VYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKS 883
 :||| ||| :|:|:||||||| ||||| |:| ||| :||| |:|
 Db 815 IYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS---PKEYTDLEVSNKS 870
 Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSAL 943
 |||| || |||:| ||| || ||| : |||:| |:| ||| || |:|
 Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPLLLPNVSAL 928
 Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT 1003
 :| |: :||| ||| |:| ||||| |:| |:| |:| ||||| |||||
 Db 929 -ESQIEMGNI VKPKVLTKEAEKKLPDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT 987
 Qy 1004 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL 1063
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 988 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL 1047
 Qy 1064 ESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNG 1123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1048 ESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNG 1107

QY 1124 LTLLILALISLFSVPVIERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
| | | | | | | | | | : | | | | | | | | | | | | | : | | | | | | | | | | | |
Db 1108 LTLLILALISLFSIPVIERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1162

RESULT 3

O8K3G8

```
ID      Q8K3G8      PRELIMINARY;      PRT;  1163 AA.
AC      Q8K3G8;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Nogo-A.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Jin W., Long M., Li R., Ju G.;
RT      "Cloning and expression of the mouse Nogo-A protein.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY114152; AAM77068.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;
```

Query Match 72.2%; Score 4277.5; DB 11; Length 1163;
Best Local Similarity 73.8%; Pred. No. 3.9e-205;
Matches 883; Conservative 108; Mismatches 154; Indels 51; Gaps 19;

QY	1	MEDLDQSPVLVSS--DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
Db	1	MEDIDQSSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEEEEEDEDEDLEELEVLERKP	60
QY	60	AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPA	119
Db	61	AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPTAPERQPSWERSPAAS---A	114
QY	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
QY	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS	225
Db	164	GSGSVDETFLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFFETAASLPSLS	223
QY	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
Db	224	PLSTVSFKEHGYLGNL SAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE	283
QY	286	MGSSFSVSPKAESAVIVANPREEII VKNKDDEEKLVSNNILHXOQELPTALTCLKVKEDEV	345

Db	284	MGSSFNKSPKGESAMLVENTKEEVI VRSKDKED-LVCSAALHNPQESPATLTQVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES	404
Db	343	MSPEKTMDFNEMKMSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
Db	399	KVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFT-SATESTAAN	457
Qy	465	IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNFFVAAQDSETDYVTTDNLTQV	524
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIHDSEADYVTTDNLSKV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGKIAYETKMDLVQTSEVMQESLYPAAQLCP	584
Db	517	TEAVVATMPEGLTPDLVQEACESELNEATGKIAYETKVDLVQTSEAIQESIYPTAQLCP	576
Qy	585	SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENPP	643
Db	577	SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVSPSPSYDGIKLEPENPP	636
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DY	703
Db	637	PYEEAMSVALKTSDAKEEIKEPESFNAAQEAEPYISIACDLIKETKLSTEPSPGFSNY	696
Qy	704	SEMAKVEQPVPDHSELVEDSSPDSEPVDFLSDDSIPDVPQKQDETVMVLKESLTETS FES	763
Db	697	SEIAKFEKSVPDHCCELVDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTEVS-ET	755
Qy	764	MIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTA	823
Db	756	VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA	814
Qy	824	VYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKS	883
Db	815	IYSNDDLLSSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS----PKEYTDLEVSNKS	870
Qy	884	EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SAL	943
Db	871	EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSVSKVPLLLPNVSAL	928
Qy	944	GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT	1003
Db	929	-ESQIEMGNIVKPKVLTKEAEKKLPSDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT	987
Qy	1004	GVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	GVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

Db 1108 GLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

08BGK7

Query Match 61.8%; Score 3658.5; DB 11; Length 1046;
Best Local Similarity 69.5%; Pred. No. 2.6e-174;
Matches 767; Conservative 108; Mismatches 148; Indels 81; Gaps 17;

Qy 257 EASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFSVSPKAESAVIVANPREEIIVKNKDE 316
 |||:|: |:| :|:|: ||| |||||: ||| |||:| | :|:|:|:|:|:
 Db 139 EASRELPERATNPFVNRESAEFSVLEYSEMSSFNKSPKGESAMLVENTKEEVIVRSKDK 198

Qy 317 EEKLVSNNILHXQQELPTALTCLVKEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376
 |: || : || | | |||:| ||| |:| || | ||| :|:| |:| ||||| |||||
 Db 199 ED-LVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKPF 257

Qy 377 ERVWEVKDSKEDS-DMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESSNDDTSFPS 435
 |: |||||: | | |:| || :|:| ||||| ||||| | ||||| |:| |||
 Db 258 EQAWEVKDTEGSRDVLAA----RANMESKVDDKKCFEDSLEQKGHGKDSSESRNENASFP 313

Qy 436 TPEGIKDRSGAYITCAPFNPAATESIATNIFPLEDPTSENXTDEKKIEEKKAQIVTEKN 495
 ||| :|| | |||| |: :||| | ||||| |||| | ||||| |:| ||| |||||
 Db 314 TPELVKDGSRAYITCDSFS-SATESTAANIFPVLEDHTSENKTDEKKIEERKAQIITEK- 371

Qy 496 TSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGT 555
 || ||||| || ||| |||||: ||| ||| ||||| ||||| ||||| ||||| |||||
 Db 372 TSPKTSNPFVVAIHDSADYVTTDNLTKVTEAVVATMPEGLTPDLVQEACESELNEATGT 431

Qy 556 KIAETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGA 615
 |||||: ||||| :||: || |||||: ||||| ||||| ||||| :|| ||
 Db 432 KIAETKMDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGA 491

Qy 616 SVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAAALQE 674
 || |||: ||| | |:| || ||||| |||||: || | |||||: || ||
 Db 492 SVAQPSASPLEVSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQE 551

Qy 675 TEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS 734
 ||||| ||||| ||||| |:|:|:|:|:| |:| ||| |||:|:|:|:| |||||
 Db 552 AEAPYISIACDLIKETKLSPEFSNYSEIAKFEKSVPDPHCELVDSSPESEPVDLFS 611

Qy 735 DDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDN 794
 |||||: ||| |:| |||: ||||| | |:| :|:|:|:|:| | | |||||: |:|
 Db 612 DDSIPEVPQTQEEAVMLMKESLTVS-ETVTQHKHKERLSASPQEVGKPYLESFQPNLHI 670

Qy 795 TKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSOSSPIEIID 854
 ||| :|: |:|:| ||| ||||| |:|:| ||||| ||| :|:|:|:| |||||
 Db 671 TKDA-ASNEIPTLTKKETISLQMEEFNTAISNDDLSSKEDKMKESSETFSOSSPIEIID 729

Qy 855 EFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE 914
 |||| |:| || :|:| |||||: ||||| || |||||: || || || ||
 Db 730 EFPTFVSAKDDS----PKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785

Qy 915 EKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPDTEKE 974
 : ||:|: |:| ||| || |:| || :| |:|:| ||||| |||||: |||||
 Db 786 AHV--SDEFSKSRSSSVKVPPLLPNVSALESGIEMGNIVKPKVLTKEAEKKLPDTEKE 842

Qy 975 DRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034
 ||| :|: |:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 843 DRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 902

Qy 1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 903 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 962

Qy 1095 LFLVDDLVDLKFVAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154
 |||:|||||
 Db 963 LFLVDDLVDLKFVAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 1022
 Qy 1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||:|||||
 Db 1023 ANKSVKDAMAKIQAKIPGLKRKAE 1046

RESULT 5

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.
 AC Q8K290;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC032192; AAH32192.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 42.7%; Score 2527; DB 11; Length 639;
 Best Local Similarity 79.5%; Pred. No. 3.6e-118;
 Matches 515; Conservative 57; Mismatches 66; Indels 10; Gaps 6;

Qy 532 MPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEA 591
 |||:|||||
 Db 1 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEA 60
 Qy 592 TPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENPPPYEEAMS 650
 |||:|||||
 Db 61 TPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPPPYEEAMS 120
 Qy 651 VSLKVSIGIKEEIKEPENINAAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710
 |:| | |||: ||| || ||||| ||||| |:|: |:|: |:|: |
 Db 121 VALKTSDAKEEIKEPESFNAAAQEAEPYISIACDLIKETKLSTEPSPEFSNYSEIAKFE 180
 Qy 711 QPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFSMIEYENK 770
 : ||| |||: |||: ||||| ||| |:| |||: ||||| | |:| :|||
 Db 181 KSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHK 239
 Qy 771 EKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL 830
 |:| | | |||||: | || |:| |:| | ||| |:|: |||||
 Db 240 ERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDL 298

Qy 831 FISKEAQIRETETFSDDSSPIEIIDFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPD 890
 ||| ::|:||||||||||||||| :|:| || :|||||||:|||||||
 Db 299 LSSKEDKMKESETFSDSSPIEIIDFPTFVSAKDDS----PKEYTDLEVS NKSEIANVQS 354

Qy 891 GAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEI 950
 || ||||:||| ||| || || | : ||:||||: |: ||| || |:|||| :| |:|
 Db 355 GANSLPCSELP CDLSFKNTYPKDEAHV--SDEF SKSRSSVSKVPLLLPNVSAL-ESQIEM 411

Qy 951 ESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGAS 1010
 :||||||| ||||:||||||||||| :|: ||:| ||||| ||||| ||||| |||||
 Db 412 GNIVKPKVLTKEAEKKLP SDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGAS 471

Qy 1011 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAIS 1070
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 472 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAIS 531

Qy 1071 EELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILA 1130
 ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
 Db 532 EELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILA 591

Qy 1131 LISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 |||||:|||||||||||||||||||:|||||||||||||||||||
 Db 592 LISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 639

RESULT 6

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
 AC Q96B16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;

Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	191	-----	190
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
		: :	
Db	191	-----ALPAA-----	195
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	196	-----	195
Qy	721	EDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG	780
Db	196	-----SEPV-----	199
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRE	840
Db	200	-----	199
Qy	841	TETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	200	-----	199
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLE	960
Db	200	-----	199
Qy	961	KEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
		: :	
Db	200	-----IRSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	234
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	235	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	294
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	295	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	354
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	355	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	392

RESULT 7

Q8BHF5

ID	Q8BHF5	PRELIMINARY;	PRT;	375 AA.
AC	Q8BHF5;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	RTN4.			
GN	RTN4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
		:	
Db	166	-----GSVDETLF-----	173
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	174	-----	173
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD	599
Db	174	-----	173
Qy	600	IVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK	659
		: :	
Db	174	-----ALPAA-----	178
Qy	660	EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL	719
Db	179	-----	178
Qy	720	VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPE	779
Db	179	-----SEPV-----	182
Qy	780	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDLFISKEAQIR	839
Db	183	-----	182
Qy	840	ETETFSDSSPIEI IDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE	899
Db	183	-----	182
Qy	900	LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS SKVLLLPPDV SALGHTQAEIESIVKPKVL	959
Db	183	-----	182
Qy	960	EKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV	1019
		: : :	
Db	183	-----IPS-----SAVVDDLLYWRDIKKTGVVFGASLFLLLSLTV	216
Qy	1020	FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN	1079
Db	217	FSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSN	276
Qy	1080	SALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV	1139
Db	277	SALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPV	336
Qy	1140	IYERHQAQIDHYLGLANKNVKDAMAKIQAQIPGLKRKAE	1178
Db	337	IYERHQAQIDHYLGLANKSVKDAMAKIQAQIPGLKRKAE	375

Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVSSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTQVTEEVVANMP EGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIA YETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD	599
Db	166	-----	165
Qy	600	IVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK	659
Db	166	-----	165
Qy	660	EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSEL	719
Db	166	-----	165
Qy	720	VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE	779
Db	166	-----	165
Qy	780	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIR	839
Db	166	-----	165
Qy	840	ETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE	899
Db	166	----- :-----GSV-----	168
Qy	900	LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDVSALGHTQAEIESIVKPKVL	959
Db	169	-----	168
Qy	960	EKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV	1019
Db	169	----- -----VVDLLYWRDIKKTGVVFGASLFLLLSLTV	197
Qy	1020	FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN	1079
Db	198	FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN	257
Qy	1080	SALGHVNCTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLIILALISLFSVPV	1139

Qy	300	VIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD	599
Db	166	-----	165
Qy	600	IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK	659
Db	166	-----	165
Qy	660	EEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL	719
Db	166	-----	165
Qy	720	VEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPE	779
Db	166	-----	165
Qy	780	GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIR	839
Db	166	-----	165
Qy	840	ETETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE	899
Db	166	----- : -GSV-----	168
Qy	900	LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVL	959
Db	169	-----	168
Qy	960	EKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLT	1018
Db	169	----- VVDLLYWRDIKKTGVVYFGASLFLLLSLT	197
Qy	1019	VFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYS	1078
Db	198	VFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYS	257
Qy	1079	NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP	1138
Db	258	NSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP	317

Qy 1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||:||||||||||||||
 Db 318 VIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 357

RESULT 10

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.
 AC Q9GM33;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 19.9 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB049853; BAB16739.1; -.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 14.6%; Score 867; DB 6; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.1e-36;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1000 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFP 1059
 :||||||||||||||||||||||||||||||||||||||:||||||||||||||
 Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHFP 60
 Qy 1060 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGA 1119
 ||||||||||||||||||||||||||||||||||||||||:||||||||||||||
 Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLRFVLMWVFTYVGA 120
 Qy 1120 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||:||||||||||||||
 Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 11

Q90638

ID Q90638 PRELIMINARY; PRT; 760 AA.
 AC Q90638;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE ChS-Rex-b.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96386034; PubMed=8793864;
 RA Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
 RA Georgiev G.P., Buchman V.L.;
 RT "Intracellular compartmentalization of two differentially spliced s-
 RT rex/NSP mRNAs in neurons."
 RL Mol. Cell. Neurosci. 7:289-303(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97183663;
 RA Ninkina N.N., Baka I.D., Buchman V.L.;
 RT "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
 RT transcripts and expression of splice variants in rat tissues."
 RL Gene 184:205-210(1997).
 DR EMBL; U17606; AAC60075.1; -.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 760 AA; 82502 MW; 465C1B429F799D5C CRC64;

Query Match 13.3%; Score 788.5; DB 13; Length 760;
 Best Local Similarity 27.7%; Pred. No. 2.4e-31;
 Matches 296; Conservative 115; Mismatches 315; Indels 341; Gaps 38;

Qy	143	PPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXXKIMDLKEQPGNT	202
		:	
Db	4	PPDPQDLLLAGTAER-W-----AAAGADEYAAGAALRDGDGA-----QQREQL	45
Qy	203	ISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEV	262
		: : : : : :	
Db	46	AFGSAREHPPVAMATA-----SPGVTASSRLFDY-----GSSSANGADSSFYT	88
Qy	263	SEKAKTLLID-----RDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVKNKDE	316
		: : : : : :	
Db	89	S-----LISDVHYTTPRDNTYFTGV-YQQENSPIPCSGSTEGFNALGHPVQDV---TGFE	139
Qy	317	EEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPF	376
		: : : :	
Db	140	SRGLFS-----LDSGIEMTPAES-----EVDKSLTDPMKVEGYKYMDI	178
Qy	377	ERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSESSNDD--TSFP	434
		: : :	
Db	179	SRPEEIK-----YQEKHDPDSEDESPDLIDEYR	206
Qy	435	STPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEK	494
		: : : : :	
Db	207	GTPIG----SGH--AAEPQRTTASEAIKA---PKEQDPLE---DKSFRDQHNASVVTAP	253

Qy 495 NTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANM---PE-----GLTP 538
 Db 254 VKITLTETPGAREATSKEASVTQPKSGLKPSHEVVPTVMVSEPEDDSPGSVTPPSSGTEP 313
 Qy 539 DLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLP 598
 Db 314 SGSESQKGKSLSEDELISAIKEAKGFSFETSEVQQS---PAV----SAEKQE QKMKPGRP 366
 Qy 599 DIVMEAPLNSAVPSA--GASVIQ-PSSSPLEASSV---NYESIKHEPENPPPYEEAMSVS 652
 Db 367 --AVPSPLDNEASSAESGDSEIELVSEDPLAAEEVLHSNYMTFSH-IGGPPP--SPASPS 421
 Qy 653 LKVSIGIKKEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQP 712
 Db 422 IQYSILREERE-----AELDSELIIESCD---ASSASEESP-----KREQD 459
 Qy 713 VPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEK 772
 Db 460 SPLMKPMVMD-----IIEKE-----ENSSR 478
 Qy 773 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDLFI 832
 Db 479 ASADYE----- 485
 Qy 833 SKEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGA 892
 Db 486 -----ASKTTE-SRMNRE-----NLADSA 503
 Qy 893 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVVALGHTQAEIES 952
 Db 504 SYLKSS-----FVAPKVSSE-----PPTSAVSTEELKERI 533
 Qy 953 IVKPKVLEKEAEKKLPDTEKEDRSPSAI-FSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
 Db 534 ILKKPIEETVNVQSKVSSKDSGKRSPALPLLPFLNKQKAINLLYWRDIKQTGIVFGSLL 593
 Qy 1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
 Db 594 LLLFSLTQFSVSVVAYLALAGLSATISFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQ 653
 Qy 1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
 Db 654 DQIQKYTDCLQLYVNSTVKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLIMAV 713
 Qy 1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 714 VSMFTLPVVYDKYQAQIDQYLGLVRTHINTVVAKIQAKIPGAKRKAE 760

RESULT 12

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.

AC Q8K4S4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Reticulon 1A.

GN RTN1 OR RTN-1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,
 RA Osumi N.;
 RT "Mosaic development of the olfactory cortex with Pax6-dependent and
 RT -independent components.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB074899; BAB96551.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 13.2%; Score 779; DB 11; Length 780;
 Best Local Similarity 30.8%; Pred. No. 7.5e-31;
 Matches 236; Conservative 108; Mismatches 227; Indels 194; Gaps 28;

QY	538	PDLVQEACESELNEVTG-----TKIAYETKMDLVQTSEVMQ-ESLYPAAQLCPSFEES	589
		: : : : : : : : : :	
Db	86	PDALDHSPSSTLKDGEACYSLSIDVCYPPREDSSAYFTGILQKENGHITTSESP--EEP	143
QY	590	EATPSPVLPDIVMEAP---LNS-----AVPSAGASVIQPSSSPLE---ASSVNY-----	632
		: : : : : : : :	
Db	144	E-TPGPSLPEVPGMEPQGLLSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDITRP	202
QY	633	ESIKHEPENPPPYEE-----AMSVSLKVSIGIKKEIKEPENINAAL-----QETEA	677
		: : : : : : : :	
Db	203	QEAKGQEEQHFGLEDKDLDFKDKGTEVSTKAEGVRAP-NQPAPVEGKLIKDHLEESTFA	261
QY	678	PYISIACDLIKETKLSAEPAPDFSDYSE----MAKVEQVPDPHSELVEDSSPDSEPVDL	732
		: : : : : : : : :	
Db	262	PYIDELSD--EQHRVSLVTAPVKITLTEIEPPLMTATQETIPEKQDLCLKPSPDTVPTVT	319
QY	733	FS---DDS-----IPDVPQKQ-----DETVMLVKESLTETSFESMIEYENKE	771
		: : : : :	
Db	320	VSEPEDDSPGVSPTPPSSGTEPSAAESQGKGSVSEDELIAAIKEA-----KGLSYETTE	372
QY	772	KLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLF	831
		: : : : : :	
Db	373	SPRPVGQVADKP-----KTKTRSGGLPTIPSPLDQEASSAESGD---	410
QY	832	ISKEAQIRETETFTSDSSPIEIIIDEFPTL-----ISSKTDSFSKLAREYTDL	877
		: : : : : :	
Db	411	-----SEIELVSEDPMASEDALPSGYVSFGHVSGPPPPSPASPSIQYSIL	454
QY	878	-----EVSHKSEIANAPDGAGSLP-----CTELPHDLS	905
		:	
Db	455	REEREAELDSELIIESCDASSASEESPKREQDSPMPKPGALDAIREETGSRATEERAPSH	514

Qy 906 LKNIQPKVEEKISFSDDFSKNKSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEK 965
 Db 515 QGPVEP--DPMLSF-----APAAALQSRPEPSS-----GDGASVPEP---PRSQQQ 555

Qy 966 KLPSDTEKEDRSPSAI-FSADLG-----KTSVVDLLYWRDIKKTGVVFGASLFL 1013
 Db 556 KPEEEAVSSSQSP TATEIPGPLGSGLM PPLPFFNKQKAIDL LYWRDIKQTGIVFGSFLLL 615

Qy 1014 LLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEEL 1073
 Db 616 LFSLTQFSVSVVAYLALAA SATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQE Q 675

Qy 1074 VQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALIS 1133
 Db 676 IQKYTDCLQLYVNSTLKE LRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLLM AVVS 735

Qy 1134 LFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 736 MFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQA KIPGAKRHAE 780

RESULT 13

Q8K0T0

ID Q8K0T0 PRELIMINARY; PRT; 780 AA.
 AC Q8K0T0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to reticulon 1.
 GN RTN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030455; AAH30455.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83572 MW; 29B47A58FC2F2027 CRC64;

Query Match 13.1%; Score 778; DB 11; Length 780;
 Best Local Similarity 30.8%; Pred. No. 8.4e-31;
 Matches 236; Conservative 108; Mismatches 227; Indels 194; Gaps 28;

Qy 538 PDLVQEACESELNEVTG-----TKIAYETKMDLVQTSEVMQ-ESLYPAAQLCPSFEES 589
 Db 86 PDALDHSPSSTLKDGE GACYTSLISDVCYPPRED SAYFTGILQKENGHIITSESP--EEP 143

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK032109; BAC27708.1; -.
 SQ SEQUENCE 643 AA; 68769 MW; 15E3335B280533F8 CRC64;

Query Match 11.8%; Score 699; DB 11; Length 643;
 Best Local Similarity 31.9%; Pred. No. 5.6e-27;
 Matches 201; Conservative 95; Mismatches 186; Indels 148; Gaps 20;

Qy	591	ATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMS	650
		: : : : :	
Db	120	ATVEVTLPN-----LRGAWPNSVMGEVTEVDSSGESDDTVIEDITEKPDSLP-----S	167
Qy	651	VSLKVGSIKEEIKPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVE	710
		: : : :	
Db	168	AAAKTS--EREIKETPS-----RETV-----	186
Qy	711	QPVPDHSSELVEDS-SPDSEPVLDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYEN	769
		: : : : : : :	
Db	187	-----RSEMCENSEQPQAQP-----ETPTQKSLEGEVASQVPNTLNEVTPEKLDMTNN	234
Qy	770	KEKLSALPP----EGG-----KPYLESFKLSLDNTKDTLLPDEVSTL--SKKEKIPLQ	816
		: : : : : : :	
Db	235	PKVCSAAPPVSLNETGFSLTVPASAKLESLLGKYVEDTDGSSPEDLMAVLTGAEEKGIVD	294
Qy	817	MEELSTAVYSNDDLFIKSEAQIRETETFSDDSPIEII DEFPTLISSKT----DSFSKLAR	872
		: : : : : : :	
Db	295	KEE-----GDVL-----EAVLEKIADFKNTLPVELLHE-SELSGSETKNIKSKYSEDSR	342
Qy	873	EYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI-----	917
		: : : : :	
Db	343	ETT-----GGAPTMSPDLEQEQLT-IRAIKELGERQAEKVQDEGISSGGKLGKQTF	391
Qy	918	-----SFSDDFSKNGSATSKVLLLLPPDVSA LGHTQAE-IESIVKPKVLEKEAEKKLPS	969
		: : : : : : : :	
Db	392	APQSGPQSSSDILEHTDVKTGSDLGIPKNPTIIKNTRIDSISSLTKTEMVNKNVLRLLS	451
Qy	970	DTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYI	1029
		: : : : :	
Db	452	D-----FPVHDLIFWRDVKKTG FVFGTTLIMLLSLAASFVISVVSYL	493
Qy	1030	ALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTI	1089
		: : : : : : :	
Db	494	ILALLSVTISFRVYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKAL	553
Qy	1090	KELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQID	1149

Db 554 KLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLVFSVPVYKYKTQID 613
 Qy 1150 HYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178
 Db 614 HYVGIARDQTKSIVEKIQAQLPGIAKKAE 643

RESULT 15

Q9BQ59

ID Q9BQ59 PRELIMINARY; PRT; 199 AA.
 AC Q9BQ59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to reticulon 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003003; AAH03003.1; -.
 DR EMBL; BC000314; AAH00314.1; -.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 11.6%; Score 688; DB 4; Length 199;
 Best Local Similarity 67.5%; Pred. No. 4e-27;
 Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

Qy 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 1047
 Db 9 KSQAIDLlyWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 68
 Qy 1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
 Db 69 QAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKF 128
 Qy 1108 AVLMMWVF'TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
 Db 129 AVLMWLLTYVGALFNGLTLLMAVVSMTFLPVVYVKHQAQIDQYLGVRTHINAVVAKIQ 188
 Qy 1168 AKIPGLKRKAE 1178
 Db 189 AKIPGAKRHAE 199

Search completed: January 22, 2004, 16:34:12
 Job time : 68.624 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:34:19 ; Search time 58.0516 Seconds
(without alignments)
4195.163 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	5815	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
2	5815	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
3	5815	98.2	1192	15	US-10-060-036-71	Sequence 71, Appl
4	5810	98.1	1192	9	US-09-789-386-2	Sequence 2, Appli
5	5810	98.1	1192	9	US-09-893-348-23	Sequence 23, Appl
6	4296.5	72.5	1163	9	US-09-893-348-18	Sequence 18, Appl
7	1495.5	25.2	373	9	US-09-789-386-6	Sequence 6, Appli
8	1495.5	25.2	373	9	US-09-765-205-6	Sequence 6, Appli
9	1495.5	25.2	373	9	US-09-893-348-24	Sequence 24, Appl
10	1495.5	275X7	373	15	US-10-060-036-72 LF	Sequence 72, Appl
11	1417	23.9	289	9	US-09-789-386-4	Sequence 4, Appli
12	1225.5	20.7	379	12	US-10-205-194-164	Sequence 164, App
13	1187	20.0	360	9	US-09-893-348-20	Sequence 20, Appl
14	931	15.7	199	9	US-09-893-348-25	Sequence 25, Appl
15	908	15.3	199	9	US-09-893-348-21	Sequence 21, Appl
16	791	13.4	777	12	US-10-205-219-93	Sequence 93, Appl
17	704	11.9	593	12	US-10-108-260A-2892	Sequence 2892, Ap
18	671	11.3	267	12	US-10-205-194-127	Sequence 127, App
19	625.5	10.6	236	9	US-09-729-674-20	Sequence 20, Appl
20	625.5	10.6	236	9	US-09-765-205-26075X7	Sequence 26075X7
21	625.5	10.6	269	15	US-10-106-698-6222	Sequence 6222, Ap
22	541.5	9.1	168	11	US-09-809-391-563	Sequence 563, App
23	541.5	9.1	168	12	US-09-882-171-563	Sequence 563, App
24	494	8.3	118	12	US-10-264-237-1568	Sequence 1568, Ap
25	340.5	5.7	1095	15	US-10-128-714-8305	Sequence 8305, Ap
26	331	5.6	66	9	US-09-758-140-20	Sequence 20, Appl
27	331	5.6	66	9	US-09-972-599A-20	Sequence 20, Appl
28	330	5.6	66	9	US-09-972-599A-22	Sequence 22, Appl
29	330	5.6	66	11	US-09-972-546-7	Sequence 7, Appli
30	311.5	5.3	98	15	US-10-050-704-179	Sequence 179, App
31	285	4.8	92	11	US-09-809-391-411	Sequence 411, App
32	285	4.8	92	12	US-09-882-171-411	Sequence 411, App
33	283.5	4.8	161	9	US-09-925-302-808	Sequence 808, App
34	276.5	4.7	1786	10	US-09-742-096-3	Sequence 3, Appli
35	275	4.6	1000	15	US-10-128-714-3305	Sequence 3305, Ap
36	274	4.6	3507	12	US-10-369-493-5784	Sequence 5784, Ap
37	273.5	4.6	2665	9	US-09-864-761-34248	Sequence 34248, A
38	273.5	4.6	3664	15	US-10-177-293-423	Sequence 423, App
39	267.5	4.5	1601	10	US-09-862-027-40	Sequence 40, Appl
40	265	4.5	1596	10	US-09-902-432-4	Sequence 4, Appli
41	263.5	4.4	2409	15	US-10-177-293-90	Sequence 90, Appl
42	262.5	4.4	6642	12	US-10-369-493-5013	Sequence 5013, Ap
43	258	4.4	1616	11	US-09-820-843A-16	Sequence 16, Appl
44	258	4.4	3913	12	US-10-334-143-45	Sequence 45, Appl
45	257.5	4.3	1781	9	US-09-738-877-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match 98.2%; Score 5815; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 3.5e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEE	EDEDLEELEVLERKPA	60	8625XG
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA		60	
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVPAP		120	
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVPAP		120	
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG		180	
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG		180	
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP		226	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP		240	
Qy	227	LSAASFKEHEYLGNLSTVLPT GTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM		286	
Db	241	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM		300	
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV		346	
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV		360	
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV		406	
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV		420	
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF		466	
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF		480	
Qy	4QF0	PILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTE		526	

Db 481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540
 Qy 527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
 Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 720
 Qy 706 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 765
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 780
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825
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 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840
 Qy 826 SNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 SNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGH 945
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALA- 959
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV 1005
 |||||||||||||||| : ||||||||||||||||||||
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLT 1125
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLT 1139
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 2

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 98.2%; Score 5815; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 3.5e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE	540

Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS SKVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS SKVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 3

US-10-060-036-71

; Sequence 71, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71

Query Match 98.2%; Score 5815; DB 15; Length 1192;
Best Local Similarity 97.2%; Pred. No. 3.5e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      |||
Db    241 LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV 346
      |||
Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 466
      |||
Db    421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 480

Qy    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
      |||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
      |||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
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Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFSDDSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLP SDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE	1192

RESULT 4

US-09-789-386-2

; Sequence 2, Application US/09789386
 ; Patent No. US20020010324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MICHALOVICH, DAVID
 ; APPLICANT: PRINJHA, RABINDER KUMAR
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30165-C1
 ; CURRENT APPLICATION NUMBER: US/09/789,386
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: US 09/359,208

Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLI SSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEI IDEFPTLI SSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIF SADLGKTSVVDLLYWRDI KKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLP SDTEKEDRSPSAIF SAE LSKTSVVDLLYWRDI KKTGV	1019
Qy	1006	VFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFRAYLES	1065
Db	1020	VFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKI PGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKI PGLKRKAE	1192

RESULT 5

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 98.1%; Score 5810; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 6.2e-284;
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRQPFAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRQPFAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
      |||:
Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      |||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
      |||
Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      |||
Db    421 DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy    467 PLLEDPTSSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 526
      |||
Db    481 PLLGDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE 540

Qy    527 EVVANMPEGLTPDLVQFACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPF 586
      |||
Db    541 EVVANMPEGLTPDLVQFACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSPF 600

Qy    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646
      |||
```

Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFSDSSPIE IDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFSDSSPIE IDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI SFSDDFS KNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI SFSDDFS KNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAI FSADLGKTSVVDLLYWRDI KKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAI FSAELSKTSVVDLLYWRDI KKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTI KELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTI KELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKI PGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKI QAKI PGLKRKAE	1192

RESULT 6

US-09-893-348-18

; Sequence 18, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

```
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18
```

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Query Match          72.5%; Score 4296.5; DB 9; Length 1163;
Best Local Similarity 74.0%; Pred. No. 7.4e-208;
Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;
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Qy      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELVLERK 58
      |||:|||| ||||| ||||| ||||| ||||| |||||:|::| ||||| |||||
Db      1 MEDIDQSSLVSSSTDSPRPAPPAFKYQFVTEPEDEEEDDEEEDDEDLEELVLERK 60

Qy     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118
      ||||| || || ||| |||:| | :| ||||| ||||| ||||| |||: || : |
Db     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy    179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
      ||| : ||||| |||||:|:| ||||| ||||| ||||| ||||| |||||
Db    167 RGSGSVDETLFALPAASEPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226

Qy    225 SPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
      |||| ||||| ||||| | :|||:| :|:| ||||: |:| :| ||| |||||
Db    227 SPLSTVSFKEHGYLGNLSAVSSSEGTTIETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy    285 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE 344
      ||||| ||| |||:| | :|:|:|:|:|:| | | : || || | |||
Db    287 EMGSSFPKGSFKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy    345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403
      ||| || | ||| :|:| ||:| ||||| |||||: ||||: | | |:| | :|:|
Db    341 VVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE 396

Qy    404 SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463
      ||||:| | |||| : |||| |:| ||||| :| | ||||| | :|||
Db    397 SKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455

Qy    464 NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTK 523
      | ||||| |||| |||||:| |||:| | ||||| || ||| ||||| |:|
Db    456 NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514

Qy    524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583
      ||| |:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574
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; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 1.2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN 240
      |||:|
Db    181 SSGSV----- 185

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
Db    186 ----- 185
```

Qy 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV 720
 Db 186 ----- 185
 Qy 721 EDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
 Db 186 ----- 185
 Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRE 840
 Db 186 ----- 185
 Qy 841 TETFSDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 Qy 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 Qy 961 KEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
 Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 Qy 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
 Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 8

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 373

; TYPE: PRT

; ORGANISM: human

US-09-765-205-6

Query Match 25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 1.2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

```
Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGN 240
      |||:|
Db    181 SSGSV----- 185

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFVSFPAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTDDNLTKVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEAMSLSLVSGIKE 660
Db    186 ----- 185

Qy    661 EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDHSELV 720
Db    186 ----- 185

Qy    721 EDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
Db    186 ----- 185

Qy    781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840
```

Db 186 ----- 185
 Qy 841 TETFSOSSPIEIIDEFPTLISSKTDSSFKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 Qy 901 PHDLSLKNIQPKVEEKISFSDDFSKNKSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 Qy 961 KEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
 V Qy 1 1 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 Qy 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
 Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 9

US-09-893-348-24

; Sequence 24, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, G

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens

50XL

US-09-893-348-24

Query Match 25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 1.2e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

```
Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGN 240
      |||
Db    181 SSGSV----- 185

Qy    241 LSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEAMSVSLKVSGIKE 660
Db    186 ----- 185

Qy    661 EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720
Db    186 ----- 185

Qy    721 EDSSPDSEPVDLFSDDISPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG 780
Db    186 ----- 185
```

Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840

Db 186 ----- 185

Qy 841 TETFSOSSPIEIIDEFPTLISSKTDSSFKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900

Db 186 ----- 185

Qy 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE 960

Db 186 ----- 185

Qy 961 KEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDDLlyWRDIKKTGVVFGASLFLLLSLTVF 1020

Db 186 -----VVDDLlyWRDIKKTGVVFGASLFLLLSLTVF 215

Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNS 1080

Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNS 275

Qy 1081 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140

Db 276 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335

Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 10

US-10-060-036-72

; Sequence 72, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; AP : Lodes, Michael J.

LERKP45

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 72

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-72

Query Match 25.2%; Score 1495.5; DB 15; Length 373;

Best Local Similarity 31.6%; Pred. No. 1.2e-67;

Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGAVVXXXXKIMDLKEQPGNTI SAGQEDFPSVLLETAASXPSLSPLSAA SFKEHEYLGN	240
Db	181	SSGSV-----	18950XA
Qy	241	LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300
Db	186	-----	185
Qy	301	IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVSSSEKAKDSFNEKRV	360
Db	186	-----	185
Qy	361	AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420
Db	186	-----	185
Qy	421	EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXTDE	480
Db	186	-----	185
Qy	481	KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL	540
Db	186	-----	185
Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	186	-----	185
Qy	601	VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	186	-----	185
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDHSSELV	720
Db	186	-----	185
Qy	721	EDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG	780
Db	186	-----	185
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELS'TAVYSNDDLFISKEAQIRE	840
Db	186	-----	185

Qy 841 TETFSDDSSPIEIIDEFPTLISSKTD SFSK LAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
 Db 186 ----- 185
 Qy 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE 960
 Db 186 ----- 185
 Qy 961 KEAEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
 Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
 Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
 Qy 1081 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
 Db 276 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
 Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
 Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 11

US-09-789-386-4

; Sequence 4, Application US/09789386
 ; Patent No. US20020010324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MICHALOVICH, DAVID
 ; APPLICANT: PRINJHA, RABINDER KUMAR
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30165-C1
 ; CURRENT APPLICATION NUMBER: US/09/789,386
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: US 09/359,208
 ; PRIOR FILING DATE: 1999-07-22
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 289
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (31)(138)

US-09-789-386-4

Query Match 23.9%; Score 1417; DB 9; Length 289;
 Best Local Similarity 99.3%; Pred. No. 7.6e-64;
 Matches 285; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 193 MDLKEQPGNTISAGQEDFPSVLLETAASXPSSLPLSAASFKEHEYLGNLSTVLPTEGTLQ 252
 |||
 Db 3 MDLKEQPGNTISAGQEDFPSVLLETAASXPSSLPLSAASFKEHEYLGNLSTVLPTEGTLQ 62

Qy 253 ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVK 312
 |||
 Db 63 ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVK 122

Qy 313 NKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD 372
 |||
 Db 123 NKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD 182

Qy 373 FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTS 432
 |||
 Db 183 FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTS 242

Qy 433 FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD 479
 |||
 Db 243 FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENKTD 289

RESULT 12

US-10-205-194-164
 ; Sequence 164, Application US/10205194
 ; Publication No. US20030134301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alistair
 ; APPLICANT: Brooksbank, Robert
 ; APPLICANT: Pinnock, Robert
 ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
 ; FILE REFERENCE: WL-A-018201
 ; CURRENT APPLICATION NUMBER: US/10/205,194
 ; CURRENT FILING DATE: 5200-07-24
 ; PRIOR APPLICATION NUMBER: GB 0118354.0
 ; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 164
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; OTHER INFORMATION: Foocen-m2 reticulon
 US-10-205-194-164

Query Match 20.7%; Score 1225.5; DB 12; Length 379;
 Best Local Similarity 28.6%; Pred. No. 4.6e-54;
 Matches 338; Conservative 17; Mismatches 22; Indels 803; Gaps 10;

Qy 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58
 |||: ||| |||| |||| |||| |||| |||| ||||: ||:: |||| |||| ||||
 Db 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEEDDEEEEDDEDEDLEEEVLERK 60

Qy 59 PAAGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
 ||||| || ||| |||: ||: |||| |||| |||| |||| ||||: ||: ||

Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYL	238
Db	167	RGS-----	169
Qy	239	GNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFSVSPKAES	298
Db	170	-----	169
Qy	299	AVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEK	358
Db	170	-----	169
Qy	359	RVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQT	418
Db	170	-----	169
Qy	419	NHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPILLEDPTSENXT	478
		:	
Db	170	-----GSVDETLF-----	177
Qy	479	DEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTP	538
Db	178	-----	177
Qy	539	DLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESESEATPSPVLP	598
Db	178	-----	177
Qy	599	DIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGI	658
		: :	
Db	178	-----ALPAA-----	182
Qy	659	KEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSE	718
Db	183	-----	182
Qy	719	LVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPP	778
Db	183	-----SEPV-----	186
Qy	779	EGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQI	838
Db	187	-----	186
Qy	839	RETETFSDDSSPIEIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT	898
Db	187	-----	186
Qy	899	ELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKV	958
Db	187	-----	186

```

Qy      959 LEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLT 1018
          :||
Db      187 -----IPS-----SAVVDLLYWRDIKKTGVVFGASLFLLLSLT 219

Qy      1019 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 1078
          |||
Db      220 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 279

Qy      1079 NSALGHVNCTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNGLTLLILALISLFSVP 1138
          |||
Db      280 NSALGHVNSTIKELRRLFLVDDLVDLKFVFLMWVFTYVGALFNGLTLLILALISLFSIP 339

Qy      1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||
Db      340 VIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 379

```

RESULT 13

US-09-893-348-20

; Sequence 20, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-893-348-20

Query Match 20.0%; Score 1187; DB 9; Length 360;

Best Local Similarity 27.7%; Pred. No. 3.7e-52;

Matches 327; Conservative 12; Mismatches 19; Indels 822; Gaps 7;

```

Qy      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
          |||
Db      1 MEDIDQSSLVSSSTDSPPPPPAFKYQFVTEPEDEEEDDEEEEDDEDEDLEELEVLERK 60

```

Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP	118
		: : : :	
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYL	238
Db	167	RGS-----	169
Qy	239	GNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMSSFSVSPKAES	298
Db	1700	-----	169
Qy	299	AVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEK	358
Db	170	-----	169
Qy	359	RVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQT	418
Db	170	-----	169
Qy	419	NHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTS NXT	478
Db	170	-----	169
Qy	479	DEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTP	538
Db	170	-----	169
Qy	539	DLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLP	598
Db	170	-----	169
Qy	599	DIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGI	658
Db	170	-----	169
Qy	659	KEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSE	718
Db	170	-----	169
Qy	719	LVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPP	778
		SAELSKTL	
Db	170	-----	169
Qy	779	EGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELSTAVYSNDDLFI SKEAQI	838
Db	170	-----	169
Qy	839	RETETFSDDSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT	898
		:	
Db	170	-----GSV---	172
Qy	899	ELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLLPDV SALGHTQAEIESIVKPKV	958

Db 173 ----- 172

Qy 959 LEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLT 1018
 |||

Db 173 -----VVDLLYWRDIKKTGVVFGASLFLLLSLT 200

Qy 1019 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 1078
 |||

Db 201 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 260

Qy 1079 NSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLTLLILALISLFSVP 1138
 |||

Db 261 NSALGHVNSTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFNGLTLLILALISLFSIP 320

Qy WO2001393Y 1.5X12DHXLGLANKNVKDAMAKIQAQIPGLKRKAE 1178
 |||

Db 321 VIYERHQVQIDHYLGLANKSVKDAMAKIQAQIPGLKRKAD 360

RESULT 14

US-09-893-348-25

; Sequence 25, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; Pn LOCATION NUMBER: IL 124500

otide30 d

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-893-348-25

Query Match 15.7%; Score 931; DB 9; Length 199;

Best Local Similarity 99.0%; Pred. No. 1.3e-39;

Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1047
 | |||

```

Db          9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGUI 68
Qy         1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
             |||
Db          69 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 128
Qy         1108 AVLMMWFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
             |||
Db          129 AVLMMWFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 188
Qy         1168 AKIPGLKRKAE 1178
             |||
Db          189 AKIPGLKRKAE 199

```

RESULT 15

US-09-893-348-21

```

; Sequence 21, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21

```

```

Query Match          15.3%; Score 908; DB 9; Length 199;
Best Local Similarity 96.3%; Pred. No. 1.9e-38;
Matches 184; Conserved 3; Mismat 4; Indels 0; Gaps 0;

```

```

Qy          988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGUI 1047
             |
Db           9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGUI 68
Qy         1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
             |||
Db          69 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKF 128

```


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OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 19.6482 Seconds
(without alignments)
2819.465 Million cell updates/sec

Title: US-09-830-972-29
Perfect score: 5923
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5815	98.2	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
2	4296.5	72.5	1163	1	RTN4_RAT	Q9jkl1 rattus norv
3	915	15.4	199	1	RTN4_MOUSE	Q99p72 mus musculu
4	791	13.4	777	1	RTN1_RAT	Q64548 rattus norv
5	787.5	13.3	776	1	RTN1_HUMAN	Q16799 homo sapien
6	626	10.6	237	1	RTNp1E00SE52	Q9es97 mus musculu
7	625.5	10.6	236	1	RTN3_HUMAN	O95197 homo sapien
8	514	8.7	545	1	RTN2_HUMAN	O75298 homo sapien
9	500	8.4	471	1	RTN2_MOUSE	O70622 mus musculu
10	324.5	5.5	865	1	CPN_DROME	Q02910 drosophila
11	320	5.4	5147	1	PCLO_HUMAN	Q9y6v0 homo sapien
12	315	5.3	5038	1	PCLO_MOUSE	Q9qyx7 mus musculu
13	299	5.0	3924	1	ANK2_HUMAN	Q01484 homo sapien
14	296.5	5.0	2468	1	MAPB_HUMAN	P46821 homo sapien
15	289	4.9	2459	1	MAPB_RAT	P15205 rattus norv
16	289	4.9	2464	1	MAPB_MOUSE	P14873 mus musculu
17	287	4.8	5120	1	PCLO_CHICK	Q9pu36 gallus gall

18	276	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
19	264.5	4.5	8545	1	ANC1_CAEEL	Q9n4m4	caenorhabdi
20	263.5	4.4	3396	1	PGCV_HUMAN	P13611	homo sapien
21	262.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
22	260.5	4.4	3381	1	PGCV_BOVIN	P81282	bos taurus
23	259.5	4.4	1828	1	MAP2_MOUSE	P20357	mus musculu
24	258.5	4.4	2805	1	MAPA_HUMAN	P78559	homo sapien
25	258	4.4	1616	1	P200_MYCGE	Q49429	mycoplasma
26	257.5	4.3	1781	1	AK12_HUMAN	Q02952	homo sapien
27	257.5	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
28	253	4.3	1189	1	YJH6_YEAST	P47035	saccharomyc
29	252	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
30	250.5	4.2	1861	1	MAP2_RAT	P15146	rattus norv
31	249.5	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
32	248	4.2	3421	1	TEGU_HSVEB	P28955	equine herp
33	244	4.1	1362	1	BRD4_HUMAN	O60885	homo sapien
34	242	4.1	1790	1	USO1_YEAST	P25386	saccharomyc
35	239	4.0	1744	1	TANA_XENLA	Q01550	xenopus lae
36	238.5	4.0	1411	1	TCOF_HUMAN	Q13428	homo sapien
37	236.5	4.0	3358	1	PGCV_MOUSE	Q62059	mus musculu
38	235.5	4.0	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
39	233.5	3.9	1087	1	NFH_MOUSE	P19246	mus musculu
40	232	3.9	1140	1	YM96_YEAST	Q04893	saccharomyc
41	131	3.9	1140	1	KI67_HUMAN	P46013	homo sapien
42	229.5	3.9	1367	1	AMYH_YEAST	P08640	saccharomyc
43	228.5	3.9	1306	1	MSB2_YEAST	P32334	saccharomyc
44	226.5	3.8	1157	1	BBC1_YEAST	P47068	saccharomyc
45	226	3.8	1379	1	YFF9_SCHPO	O14066	schizosacch

ALIGNMENTS

RESULT 1

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine)
DE protein C homolog) (RTN-5) (Myo43 protein)
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans."
RL Nature 403:383-384(2000).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., | rgren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX =21069055; PubMed=11201742; --- 1412
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.

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 CC -----

DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.
 DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.

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DR      EMBL; AB015639; BAA83712.1; -.
DR      EMBL; AF077050; AAD27783.1; -.
DR      EMBL; AF177332; AAG17976.1; -.
DR      EMBL; AB020693; BAA74909.1; -.
DR      EMBL; BC001035; AAH01035.1; -.
DR      EMBL; BC007109; AAH07109.1; -.
DR      EMBL; BC014366; AAH14366.1; -.

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Query Match 98.2%; Score 5815; DB 1; Length 1192;
Best Local Similarity 97.2%; Pred. No. 2.2e-216;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKSAESAVIVANPREEIIIVKNKDEEEKLVSNNI LHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKSAESAVIVANPREEIIIVKNKDEEEKLVSNNI LHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705

RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129258; PubMed=10667796;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A.A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.
 DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding activity; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 FT VARSPLIC 965 975 /FTId=VSP_005656.
 FT AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).
 FT /FTId=VSP_005657.
 FT VARSPLIC 173 975 Missing (in isoform 2).
 FT /FTId=VSP_005658.
 FT VARSPLIC 192 975 Missing (in isoform 4).
 FT /FTId=VSP_005659.
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 72.5%; Score 4296.5; DB 1; Length 1163;
 Best Local Similarity 74.0%; Pred. No. 4.2e-158;
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

QY 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58
 |||:|||| ||||| ||||| ||||| |||||:||||:|||||||
 Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEDEDLEEEVLERK 60
 QY 59 PAAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
 ||||| || || ||| |||: || :| ||||| ||||| ||||| |||||: || : |
 Db 61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 QY 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 QY 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224
 ||| : |||| |||||: ||||| ||||| ||||| ||||| |||||
 Db 167 RGSGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
 QY 225 SPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLTEFSELEYS 284

Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA-----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPPFFVAAQDSETDYVTTDNLTK	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSIGKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIEKESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDFPPTLISSKTDSFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLSSKEDKIKESETFSDDSPIEIIDFPPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVS	942
Db	871	SEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122


```

CC      transmembrane domains (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms may be produced;
CC          Name=1;
CC          IsoId=Q99P72-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF326337; AAK08076.1; -.
DR      EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; ISS.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding activity; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN      1      25      CYTOPLASMIC (Potential).
FT      TRANSMEM      26      50      POTENTIAL.
FT      DOMAIN      51      137      LUMENAL (Potential).
FT      TRANSMEM      138      162      POTENTIAL.
FT      DOMAIN      163      199      CYTOPLASMIC (Potential).
FT      DOMAIN      12      199      RETICULON.
SQ      SEQUENCE      199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

```

```

Query Match      15.4%; Score 915; DB 1; Length 199;
Best Local Similarity 97.4%; Pred. No. 3.3e-29;
Matches 186; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 1047
      | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 68

QY      1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKF 1107
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKF 128

QY      1108 AVLMMWFVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
      ||||||||||||||||||||||||||||:||||||||||||||||||:|||||||
Db      129 AVLMMWFVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQ 188

QY      1168 AKIPGLKRKAE 1178
      |||||||||
Db      189 AKIPGLKRKAE 199

```

RESULT 4

RTN1_RAT

ID RTN1_RAT STANDARD; PRT; 777 AA.
AC Q64548; Q64547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN RTN1 OR NSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-
RT rex/NSP mRNAs in neurons.";
RL Mol. Cell. Neurosci. 7:289-303(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN NEUROENDOCRINE SECRETION OR IN
CC MEMBRANE TRAFFICKING IN NEUROENDOCRINE CELLS.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (BY
CC SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN1-B; Synonyms=S-RexB;
CC IsoId=Q64548-1; Sequence=Displayed;
CC Name=RTN1-S; Synonyms=S-RexS;
CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC TYPES.
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC HINDBRAIN.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17604; AAC53046.1; -.
DR EMBL; U17603; AAC53045.1; -.
DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 604 624 POTENTIAL.
 FT TRANSMEM 727 747 POTENTIAL.
 FT DOMAIN 590 777 RETICULON.
 FT DOMAIN 610 613 POLY-LEU.
 FT VARSPLIC 1 569 Missing (in isoform RTN1-S).
 FT /FTid=VSP_005647.
 FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-S).
 FT /FTid=VSP_005648.
 SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 13.4%; Score 791; DB 1; Length 777;
 Best Local Similarity 26.6%; Pred. No. 1e-23;
 Matches 290; Conservative 129; Mismatches 308; Indels 364; Gaps 39;

QY 134 PEDDEPPARPPPPPPASVSPQAE-PVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKI 192
 | : : | | : | | | | : | |
 Db 5 PDLQDEPLSPANPGSQLFGGRGEGEEATPKGARPAQQDGEPAWGS--GAGAGVVS----- 57

QY 193 MDLKEQPGNTISAGQEDFPSVLLETA----ASXP-SLSPLSAASFKEHE---YLGNLSTV 244
 : : | | : | | : | : | : | : | : | :
 Db 58 -----SRGLCSGPARSPVAMETASTGVAAPDALDHSSSPTLKDGEACYSLSIDI 110

QY 245 L--PTE-----GTLQE-----NVSEASKEVSEKAKTLLIDRLTEFSELEYSEMGSFS 291
 | | | | : | : : | : | : | : | : | :
 Db 111 CYPRED SAYFTGILQKENGHITTSESPEELGTPGPS-LPEVPGTEPHGLLSSDSGIEMT 169

QY 292 VSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKA 351
 : | : : : : : : : : : : : : : : : :
 Db 170 PAESTEVNKILADPLDQ----- 186

QY 352 KDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCF 411
 | : | : | | : | | : | | |
 Db 187 -----MKAFAECKYIDITRPQEAQGQEEQSPGL----- 213

QY 412 ADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATES--IATNIFPLL 469
 : | | : : : : : | | : | | : | : | :
 Db 214 -----EDKDLDFKDKDSEVSTKPEGVH-----APNQPSPVEGKLIKDNLF--- 253

QY 470 EDPTSENXTDEKKIEEKKAQIVTE--KNTSTKTSNPPFFVAAQDSETDYVTTDNLTKVTEE 527
 | : | | | : : : | | | : | | : :
 Db 254 EESTFAPYIDELSDEQHRMSLVTA PVKITLTEIGPPVMTATHET----- 297

QY 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFE 587
 : | | | | | | | | | : | : | :
 Db 298 ----IPE-----KQDL-----CLKPSPDTPVPTVT 317

QY 588 ESEA---TPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSP-----LEASSVNYESI KH 637
 | | : | | | : | | | : | | | : : | :
 Db 318 VSEPEDDSPG SVTP-----PSSGTEPSAAESQKG SVSEDELIAAIKEAKGLSYET--- 368

QY 638 EPENPPPYEEAMSVSLKVSGIKEEIKE-----PENINAALQETEAPYISIACDLIKET 690
 | : | | : | : : | : : : | : | : : | :
 Db 369 -TESPRPVGQAAD-----RPKVKARSGLP TIPSLLDQEASSAESGDSEI--ELVSED 417

Qy 691 KLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM 750
 Db 418 PMASEDALP-SGYVSFGHVSGPPP-----SPAS-----PSIQYSILREEREAE 459

Qy 751 LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK 810
 Db 460 LDSELIIESCDASSASEESPKREQDSPPM--KPGV-----LD-----AIREETSSRATE 506

Qy 811 EKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIE---IIDEFPTLISSKTDSF 867
 Db 507 ERAP-----SHQGPVEPDPILSFTPTVLQSRPE-- 534

Qy 868 SKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFS KNG 927
 Db 535 -----PSSGDGAPVPEPP-----KSQQQKPEEEAVSS---SQSP 565

Qy 928 SATSKVLLLPPDV SALGHTQAEIESIVKPKVLEKEAEKKLP SDTEKEDRSPSAIFSADLG 987
 Db 566 AAT-----EIPGPLGSDLVPPLPFFN---- 586

Qy 988 KTSVVDLLYWRDIKKTGVVFGASL FLLL SLTVFSIVSVTAYIALALLSVTISFRIYK GVI 1047
 Db 587 KQKAIDLLYWRDIKQTGIVFGSFL LLL FSLTQFSVSVVAYLALAL SATISFRIYKSVL 646

Qy 1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKF 1107
 Db 647 QAVQKTDEGHPFKAYLELEITLSQE QIQYTDCLQLYVNSTL KELRRLFLVQDLVD SLKF 706

Qy 1108 AVLMMWFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1167
 Db 707 AVLMWLLTYVGALFNGLTLLLMAVVSMTLPVVVYVKHQAQVDQYLGLVRTHINTVVAKIQ 766

Qy 1168 AKIPGLKRKAE 1178
 Db 767 AKIPGAKRHAE 777

RESULT 5

RTN1_HUMAN

ID RTN1_HUMAN; STANDARD; PRT; 776 AA.
 AC Q16799; Q16800; Q16801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Reticulon 1 (Neuroendocrine-specific protein).
 GN RTN1 OR NSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=93293865; PubMed=7685762;
 RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
 RA Ramaekers F.C.S., Van de Ven W.J.M.;

RT "Cloning and expression of alternative transcripts of a novel
RT neuroendocrine-specific gene and identification of its 135-kDa
RT translational product.";
RL J. Biol. Chem. 268:13439-13447(1993).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96429995; PubMed=8833145;
RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT "Genomic organization of the human NSP gene, prototype of a novel gene
RT family encoding reticulons.";
RL Genomics 32:191-199(1996).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=98228245; PubMed=9560466;
RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA Roebroek A.J., van de Velde H.J., Ramaekers F.C., Broers J.L.;
RT "Neuronal differentiation is accompanied by NSP-C expression.";
RL Cell Tissue Res. 292:229-237(1998).
CC -!- FUNCTION: MAY BE INVOLVED IN NEUROENDOCRINE SECRETION OR IN
CC MEMBRANE TRAFFICKING IN NEUROENDOCRINE CELLS.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=RTN1-A; Synonyms=NSP-A;
CC IsoId=Q16799-1; Sequence=Displayed;
CC Name=RTN1-B; Synonyms=NSP-B;
CC IsoId=Q16799-2; Sequence=VSP_005644;
CC Name=RTN1-C; Synonyms=NSP-C;
CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC -!- PTM: ISOFORMS RTN1-A AND RTN1-B ARE PHOSPHORYLATED.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; L10333; AAA59950.1; -.
DR EMBL; L10334; AAA59951.1; -.
DR EMBL; L10335; AAA59952.1; -.
DR PIR; A46583; A46583.
DR PIR; I60904; I60904.
DR Genew; HGNC:10467; RTN1.
DR MIM; 600865; -.
DR GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; TAS.
DR GO; GO:0004871; F:signal transducer activity; NAS.
DR GO; GO:0030182; P:neuron differentiation; TAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.
KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW Phosphorylation.
FT TRANSMEM 603 623 POTENTIAL.
FT TRANSMEM 726 746 POTENTIAL.
FT DOMAIN 589 776 RETICULON.
FT DOMAIN 609 612 POLY-LEU.
FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
FT /FTId=VSP_005644.
FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
FT /FTId=VSP_005645.
FT VARSPLIC 569 588 GPGPLGPGAPPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT KSQ (in isoform RTN1-C).
FT /FTId=VSP_005646.
SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 13.3%; Score 787.5; DB 1; Length 776;
Best Local Similarity 31.9%; Pred. No. 1.4e-23;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

Qy 588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQSSSPLE---ASSVNY---- 632
| | | | | : | : | : | : | : |
Db 141 EELGTPGPSLPDVPGLIESRGLFSSDSGIEMTPAESTEVNKLADPLDQMKAEAYKYIDIT 200
Qy 633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKEEIKEPENINAAL-----QET 675
| : | | : : | : | : | | : : | : |
Db 201 RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKI IKDHILLEEST 259
Qy 676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722
| | | | | | : | | | : : : : | : :
Db 260 FAPYID---DLSEEQRRAPIITPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309
Qy 723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMLVKESLTETSF 761
| | | : | | | | : | | : : | :
Db 310 PSPDTPVTVTVSEPEDDSPGSITPPSSGTEPSAAESQKGKSI SEDELITAIKEA----- 363
Qy 762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKI PLQMEELS 821
: | | | : : | : | | | : : :
Db 364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403
Qy 822 TAVYSNDDLFI SKEAQIRETETFS DSSPIEII DEFP---TLISSKTDSFS----- 868
: : | | | | : | | : | | |
Db 404 SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP 444
Qy 869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921
: | | : | : : | : : | : | | | | |
Db 445 ASPSIQYSILREEREAE L DSELI I E SCDASSAS-----EESPKREQDSPPMKPSALD 496
Qy 922 DF-----SKNGSATS K VLL-----LPPDV SALGHTQAEIESIVKP 956
| : | | | | | | | | | : | : |
Db 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL-----EPETPMLP 551
Qy 957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001
: | : : : | : | : | | | | |
Db 552 -----RKPEEDSSSNQSPAATKGPGPLGPGAPPPLLF---LNKQKAIDL YWRDIK 599
Qy 1002 KTG VVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHFPRA 1061


```

Db          600  QTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTEDEGHPFKA 659
Qy          1062 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1121
Db          660  YLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLMWLLTYVGALF 719
Qy          1122 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
Db          720  NGLTLLLMVVSMFTLPVVVYVKHQAQIDQYLGLVRTHINAVVAKIOAKIPGAKRHA 776

```

RESULT 6

RTN3 MOUSE

ID RTN3 MOUSE STANDARD; PRT: 237 AA.

AC Q9ES97;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon protein 3.

GN RTN3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;

RT "Cloning and expression profile of a novel mouse cDNA encoding a human

RT RTN3 homolog.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

CC reticulum (Potential).

CC -!- SIMILARITY: Contains 1 reticulon domain.

```
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```

DR EMBL; AF195940; AAG31360.1; -.

DR MGD; MGI:1339970; Rtn3.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

KW Transmembrane; Endoplasmic reticulum.

FT TRANSMEM 69 89 POTENTIAL.

FT TRANSMEM 167 187 POTENTIAL.

FT	DOMAIN	49	237	RETICULON.
----	--------	----	-----	------------

SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

Query Match 10.6%; Score 626; DB 1; Length 237;

Best Local Similarity 53.2%; Pred. No. 5.1e-18;

Matches 125; Conservative 41; Mismatches 53; Indels 16; Gaps 4;

Qy 960 EKEAEKKLPS-DTEKEDRSPSAIFSAD-----LGKTS-----VVDLLYWRDIKKTG 1004
 | | : | | : | | : | | | | : | | : | | : | | :
 Db 3 ESSAATQSPSVSSSSSSGAEPSALGGGGSPGACPALGAKSCGSSCAVHDLIFWRDVKKTG 62

Qy 1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 1064
 | | : | : | | | | : | : | | | | | | : | | : | | : | | : | | :
 Db 63 FVFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRVYKSVIQAVQKSEEGHPFKAYLD 122

Qy 1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL 1124
 : : : | | | : | : | | : | : | | | : | | | | | | : | | : | | : | | :
 Db 123 VDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGI 182

Qy 1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178
 | | | | : : | | : | : | : | | | : | : | : | | : | : | : | : | : | : | :
 Db 183 TLLILAEELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 237

RESULT 7

RTN3_HUMAN

ID RTN3_HUMAN STANDARD; PRT; 236 AA.
 AC O95197;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
 DE protein II) (NSPLII).
 GN RTN3 OR NSPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Retina;
 RX MEDLINE=99265974; PubMed=10331947;
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene
 RT structure and chromosomal localization to 11q13.";
 RL Genomics 58:73-81(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
 RT "Cloning and expression analysis of a cDNA encoding a novel
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
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 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.
 DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.
 DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 10.6%; Score 625.5; DB 1; Length 236;
 Best Local Similarity 54.8%; Pred. No. 5.4e-18;
 Matches 119; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

QY 963 AEKKLPSTDEKEDRSPSAIFSDALGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022
 || | : : : ||::|||:|||| ||| :| :|||| ||:

Db	20	AEPSAPGGGGSPGACPALGTKSCSSCAVHDLIFWRDVKKTGTFVGTTLIMLLSLAAFSV	79
Qy	1023	VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPFRAYLESEVAISEELVQKYSNSAL : : : : : : : : : :: : : :	1082
Db	80	ISVVSYLILALLSVTISFRIYKSVIQAQVKSEEGHPFKAYLDVDITLSSEAFHNMYNAAM	139
Qy	1083	GHVNCTIKELRRLFLVDDLVDLSLKFAVLMMWVFITYVGALFNGLTLILLIALLISLFSVPVIYE : : : : : : : : : : ::	1142
Db	140	VHINRALKLIIRLFLEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVPPIVYE	199
Qy	1143	RHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE ::: : : : : : :	1178
Db	200	KYKTQIDHYVGIARDOTKSIVEKIQAKLPGIKKKAE	236

RESULT 8

RTN2 HUMAN

```

ID      RTN2_HUMAN          STANDARD;          PRT;      545 AA.
AC      075298; 060509;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE      protein 1) (NSPLI).
GN      RTN2 OR NSPL1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC      TISSUE=Lung carcinoma;
RX      MEDLINE=98360096; PubMed=9693037;
RA      Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
RT      "cDNA cloning, genomic organization, and expression of the human RTN2
RT      gene, a member of a gene family encoding reticulons.";
RL      Genomics 51:98-106(1998).
RN      [2]
RP      SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
RC      TISSUE=Brain;
RX      MEDLINE=98191726; PubMed=9530622;
RA      Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT      "Molecular cloning of a novel mouse gene with predominant muscle and
RT      neural expression.";
RL      Mamm. Genome 9:274-282(1998).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC      reticulum (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=RTN2-A;
CC      IsoId=075298-1; Sequence=Displayed;
CC      Note=Isoform RTN2-C is produced by alternative initiation at
CC      Met-341 of isoform RTN2-A;
CC      Name=RTN2-B;
CC      IsoId=075298-2; Sequence=VSP_005649;
CC      Event=Alternative initiation;
CC      Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced

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CC  -!- SIMILARITY: Contains 1 reticulon domain.
CC  -----
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CC  -----
DR  EMBL; AF038537; AAC14906.1; -.
DR  EMBL; AF038537; AAC14907.1; -.
DR  EMBL; AF038538; AAC14908.1; -.
DR  EMBL; AF038539; AAC14909.1; -.
DR  EMBL; AF093624; AAD13195.1; -.
DR  MGD; MGI:107612; Rtn2.
DR  InterPro; IPR003388; Reticulon.
DR  Pfam; PF02453; Reticulon; 1.
DR  PROSITE; PS50845; RETICULON; 1.
KW  Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT  TRANSMEM 295 315 POTENTIAL.
FT  DOMAIN 272 471 RETICULON.
FT  VARSPLIC 1 267 Missing (in isoform 2).
FT  /FTid=VSP_005650.
FT  VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).
FT  /FTid=VSP_005651.
SQ  SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

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```

Query Match          8.4%; Score 500; DB 1; Length 471;
Best Local Similarity 29.3%; Pred. No. 8.3e-13;
Matches 159; Conservative 83; Mismatches 177; Indels 124; Gaps 16;

```

```

QY 676 EAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD-SEPVDL-F 733
    |||      | | | | | : | : | : | : | : | : | : | : | : | : |
Db 13 EAP-----STASSTPDSTEGGNDSDSFRELHTAREFSEDEEE--ETTSQDWGTPRELTF 64

QY 734 S-----DDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780
    |      ||| : | : | : | : | : | : | : | : | : | : |
Db 65 SYIAFDGVVGSGGRRDSVVRPRPQGRSVSEPRDPPQQSGLGDSLESIPSLSQSPPEGR 124

QY 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE 840
    | |      | : | | | : | : | : | : | : | : | : | : |
Db 125 GDP-----DPVPPAE---RPLEELRLRLDQLG-----WVVR SAGSGE 158

QY 841 TETFS DSSPIEI IDEFPTLISS----KTDFS KLARE-YTDLEV-----SHKSEIAN 887
    | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 159 DSATSSSTPLE--NEEPDGLEASEAGEETNLELRLAQSLHLQLEVLTPQLSPSSGTPQAH 216

QY 888 APDGAGSLPCTELPHDLSL QPKVEEKISFSDDFS KNGSAZ8KVL LPPDV SALGHTQ 947
    | |      | | | | | : | | | : | : | : | : | : | : |
Db 217 TPSPQRSQDSNSGPDDEPLLNV---VEEH-----WRLLEQEPITAQCLDST 259

QY 948 AEIESIVKPKVLEKEAEKKLPDSTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVF 1007
    : | : : | : |      | | | | | : | : | : | : |
Db 260 DQSEFMLEPLLL-----VADLLYWKDTRTSGAVF 288

QY 1008 GASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEV 1067

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      : || | ||||| |::| | || |:: |::: | :||:|::: ::
Db      289 TGLMASLLCLLHFSIVSVAHLALLGLCATISLRVYRKVLQAVHRGDGTNPFGAYLDMDL 348
Qy      1068 AISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLL 1127
      :: | :: | || | :|| |||:|||||| |:: |:: |::|:|||||:
Db      349 TLTREQTERLSQQIASHVVSTATQLRHFFLVEDLVDSLKLALLFYILTFVGAIFNGLTLV 408
Qy      1128 ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KR 1175
      || ::||:|::|: |::| ||| |:: |:: |::|:|||||
Db      409 ILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGTLAPTASVSGSKA 468
Qy      1176 KAE 1178
      |||
Db      469 KAE 471

```

RESULT 10

CPN_DROME

```

ID      CPN_DROME      STANDARD;      PRT;      865 AA.
AC      Q02910;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Calphotin.
GN      CPN OR CAP.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Canton-S;
RX      MEDLINE=93165729; PubMed=8094559;
RA      Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
RT      "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Canton-S;
RX      MEDLINE=93165730; PubMed=8434015;
RA      Ballinger D.G., Xue N., Harshman K.D.;
RT      "A Drosophila photoreceptor cell-specific protein, calphotin, binds
RT      calcium and contains a leucine zipper.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
CC      !- FUNCTION: Might function as a calcium-sequestering "sponge" to
CC      regulate the amount of free cytoplasmic calcium. It binds 0.3 mole
CC      of Ca(2+) per mole of protein.
CC      !- SUBUNIT: Homodimer (Probable).
CC      !- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.
CC      !- TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF
CC      COMPOUND EYES AND OCELLI.
CC      !- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL
CC      DEVELOPMENT.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
 DR EMBL; L02111; AAA28405.1; -.
 DR EMBL; L05080; AAA28420.1; -.
 DR PIR; A47282; A47282.
 DR PIR; A47283; A47283.
 DR FlyBase; FBgn0010218; Cpn.
 DR GO; GO:0005509; F:calcium ion binding activity; IDA.
 KW Calcium-binding.
 FT CONFLICT 36 36 A -> AVAPAVVA (IN REF. 2).
 FT CONFLICT 43 43 I -> T (IN REF. 2).
 FT CONFLICT 64 64 I -> V (IN REF. 2).
 FT CONFLICT 76 76 T -> A (IN REF. 2).
 FT CONFLICT 100 100 P -> PP (IN REF. 2).
 FT CONFLICT 126 127 VQ -> AP (IN REF. 2).
 FT CONFLICT 154 154 I -> V (IN REF. 2).
 FT CONFLICT 160 160 S -> T (IN REF. 2).
 FT CONFLICT 534 534 A -> E (IN REF. 2).
 FT CONFLICT 699 699 I -> T (IN REF. 2).
 FT CONFLICT 703 703 V -> L (IN REF. 2).
 FT CONFLICT 721 721 D -> E (IN REF. 2).
 SQ SEQUENCE 865 AA; 84781 MW; 2110417E0B0E7CFE CRC64;

Query Match 5.5%; Score 324.5; DB 1; Length 865;
 Best Local Similarity 22.3%; Pred. No. 9.6e-06;
 Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
 | : ||| | | ||: | || | : | | | : | | : |
 Db 9 PVSAPVAAPV-TPSAVAAPVQVVSPAAPVAPAAPIAVTPVAPPPTLASVQPATV--TIP 65

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAP----APAAPP--ST 172
 ||:|::||:|:| || | |||: || : || | || || : |
 Db 66 APAPIAAASVTP---VASVAPPVVAAPTPPAA-SPVSTPVAVAQIPVAVSAPVAPPVAAT 121

Qy 173 PAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232
 | : : | : | | || | : || | : || | : || : |
 Db 122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160

Qy 233 KEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292
 | : | | | : : | : : | : : | : : | : : |
 Db 161 -----PPVVPANTT---VPVAAPVAAVPAAPVVPVAPVLAP-----AV 194

Qy 293 SPKAESAVIVAN-----PREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVEDEVVS 347
 : | : | : | | || | : | : | : | : | : | : |
 Db 195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234

Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407
 : | : | : | | | | | : : : : : : : : : |
 Db 235 T---KPLAAAEFVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

Qy 408 KKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467
 || : : | : | || ||

```

Db      281 -----ASTEPPV---AAATLTAPETPAL----- 301
Qy      468 LLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTDNLTQVTEE 527
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      302 -----APVVAESQ-----VAA-----NTVVATPP 320
Qy      528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579
          | | | : | : | : | | | : | | | : | | | : | | | : | | |
Db      321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371
Qy      580 -AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHE 638
          | | : : | : | | | : : | | | : | | | : | | | : | | |
Db      372 PATLAVTDPDVTASAVPELPPVIAAPSPVSAVAETPVDLAPPVLPVAAEPVPAVVAEET 431
E
Qy      s639 PENPPPYEAMS SV-SLKVSGIKKEIKEPENINAALQETEAPYISIACDLIKET PA 697
          | | | | : : : | : : | | : | | : | | : | | : | | : | |
Db      432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAAPIVSTPPTTASVPETTAPPA 491
Qy      698 P-----DFSDYSEMAKVEQVPDHSSEL-----VEDSSPDSEPVDLFSDDSIP--DVPQK 744
          | | | | | : | | | : | | : | | : | | : | | : | |
Db      492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDL 550
Qy      745 QDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804
          : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      551 LEQTTSPVAEEAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603
Qy      805 STLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLI 860
          | : | | | : : : | | | | : | | | | | | | | | | | | |
Db      604 SLATPTEPIPVEAPVVIQEAVDAV-----EVPVTETST---SIP-ETTVEFPEAV 649
|
Qy      861 SSKTDSFSKLA -SHKSEIANAPDGAGSLPCTELP-----HDL$1 906
          : | | | : | : : : | | | | | | | | | | | | | | | | |
Db      650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701
Qy      907 KNIQPKVEEKISFSDDFSKNGSATSKVLL----LP-----PDVSALG----- 944
          | | | : : : : : : : : : : : : : | | | | | | | | |
Db      702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760
Qy      945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSadLGKTSVVDLLY 996
          : | | | : | | : | | | : | : : | | | | : | : | |
Db      761 ITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814
Qy      997 WRDIKKTGV 1005
          | | : : | |
Db      815 -RDLQTTDV 822

```

RESULT 11

PCLO_HUMAN

```

ID   PCLO_HUMAN      STANDARD;          PRT;   5147 AA.
AC   Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Piccolo protein (Aczonin) (Fragments).
GN   PCLO OR ACZ OR KIAA0559.
OS   Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-759 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 RN [2]
 RP SEQUENCE OF 552-4404 FROM N.A.
 RA Kraemer J., Wollam C., Wohldmann P., McGrane B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RN [4]
 RP SEQUENCE OF 4405-4439 FROM N.A.
 RC TISSUE=Placenta; 75XI a A., Kotani H., TP KD 442850XS
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., AbY ., Mullahy S-59XP2113
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 4405-5147 FROM N.A.
 RA Kalicki J., Elliott G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle

```

CC      trafficking (By similarity).
CC      -!- SUBUNIT: Interacts with Rabac1/Pral and profilin (By similarity).
CC      -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
CC      synaptic junctions (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9Y6V0-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
CC      VSP_003926, VSP_003927;
CC      Note=No experimental confirmation available;
CC      -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      -!- SIMILARITY: C          C2 domains.                      KNY 2003
CC      -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y19188; CAB60727.1; -.
DR      EMBL; AC004903; AAD20936.1; -.
DR      EMBL; AC004886; AAD21789.1; -.
DR      EMBL; AB011131; BAA25485.1; -.
DR      EMBL; BC001304; AAH01304.1; -.
DR      EMBL; AC004082; AAB97937.1; -.
DR      PIR; T00634; T00634.
DR      HSSP; P04410; 1A25.
DR      Genew; HGNC:13406; PCLO.
DR      MIM; 604918; -.
DR      GO; GO:0005856; C:cytoskeleton; NAS.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding activity; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . .; ISS.
DR      GO; GO:0005522; F:profilin binding activity; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001565; Synaptotagmin.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat; Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      400      465      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT      P-A-K-P-Q-P-Q-Q-P-X.
FT      ZN_FING      499      523      C4-TYPE (POTENTIAL).

```

FT	ZN_FING	969	992	C4-TYPE (POTENTIAL).
FT	NON_CONS	1010	1011	
FT	DOMAIN	2300	2325	POLY-PRO.
FT	DOMAIN	4391	4442	PDZ.
FT	DOMAIN	4544	4633	C2 DOMAIN 1.
FT	DOMAIN	5031	5121	C2 DOMAIN 2.
FT	VARSPPLIC	4404	4404	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
FT				QTGKLM EG (in isoform 2).
FT				/FTId=VSP_003923.
FT	VARSPPLIC	4534	4534	K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
FT				/FTId=VSP_003924.
FT	VARSPPLIC	4576	4576	G -> GQVMVVQNAS (in isoform 2).
FT				/FTId=VSP_003925.
FT	VARSPPLIC	4757	4761	TAHKS -> SKRRK (in isoform 2).
FT				/FTId=VSP_003926.
FT	VARSPPLIC	4762	5147	Missing (in isoform 2).
FT				/FTId=VSP_003927.
SQ	SEQUENCE	5147 AA;	563537 MW;	CD5D84990498CD3C CRC64;

Query Match 5.4%; Score 320; DB 1; Length 5147;
 Best Local Similarity 21.8%; Pred. No. 0.00013;
 Matches 260; Conservative 152; Mismatches 440; Indels 340; Gaps 61;

Qy	8	PLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAP	67
		: : : :	
Db	260	PSLPSPSKPPIQQPTPGKPPAQPGHEKSQPG-----PAKPPAQPSGLT	303
Qy	68	VPTAPAAGA---PLMDFGNDFVPPAPRGPLPAAPPV-----	100
		:	
Db	304	KPLAQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKALAQPPGV	361
Qy	101	--APERQPSWDPSFVSSTVPAPSPLS-----AAAVSPSKLPEDDEPPA-----RPP	144
		: : : : :	
Db	362	GKTPAQPG-PAKPPTQQVGTGPKPLAQPGQLQSPAKAPGPTKTPAQTKPPSQPGSTKPP	420
Qy	145	P--PPPASVSPQAEPVWTPPAPAP-AAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGN	201
		: : :	
Db	421	PQQPGPAKPSPPQPGSTKPPSQPGSAKPSA-----QQPSP	456
Qy	202	TISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKE	261
		: : : : : : :	
Db	457	AKPSAQQ-FTKPVSQTGFGKPLQPPTVSPSAKQPPSQGLPKTICPL-----CNTTELLH	510
Qy	262	VSEKA-----KTL LI-----DRDLTEFSE-----LEYSEMGSFSVSPKA----	296
		: : : : :	
Db	511	VPEKANFNTCTECQTTVCSLCGFNPNPHLTEAKEWLCLNCQMKRALGGDLAPVPSSPQPK	570
Qy	297	-----ESAVIVANPREEIIVKNKDDEEEKLVSNNILHXQQEL-----PTALTCLKVKED	343
		: : : :	
Db	571	LKTAPVTTSVAVSKSSPQQQTSPKKDAAPK-----QDLSKAPEPKKPPPLVKQP	620
Qy	344	EVVSSEKAK-----DSFNEKRVAVEAPMREE-----YADFKPFERVWEVKDSKEDSDM	391
		: : : : : :	
Db	621	TLHGSPSAKAKQPPEADSLSKPAPPKEPSVPSEQDKAPVADDKP----KQPKMVKPTTDL	676
Qy	392	LAAGGKIESNLESKVD---KKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYI	448
		: : : : : : : :	

Db 677 VSS-----SSATTKPDIPSSKVQSQAEKTTPLKTDSSAKPSQSFPPPTGEKV----- 723
 Qy 449 TCAPFN-----PAATESIATNIFPLLE-----DPTSENXTDEKKIEEKKAQIVTEKN 495
 ||: ||: |:: | | || :|| | |||
 Db 724 --TPFDSKAIPRPASDSKIISHPGPSSESKGQKQVDPV-----QKKEEPKKAQTKMSPK 775
 Qy 496 TSTK-----TSNPFFVAAQDSETDYVTTD-----NLTKVTEEVVANMPEGLT 537
 | | | | : || :| : |
 Db 776 PDAKPMPKGSPPTPPGPRPTAGQTVPTPQQSPKPQEQRSLNLSITD---APKSQPTT 832
 Qy 538 PDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA--AQLCPSFEESEATPSP 595
 | || ||| : | | : | : | : | : |
 Db 833 P---QET-----VTGKLFGFGASI-FSQASNLISTAGQPGPHSQSGPGAPMKQA-PAP 880
 Qy 596 VLPDIVMEAPLNSA-VPSAGASVI-----QPSSSPLEASSVNYESIK--HEPENPPPY 645
 | :| | | | :| | : :| : |||
 Db 881 SQPPTSQGPPKSTGQAPPAPAKSIPVKKETKAPAAEKLKPAEQAPTVKRTETEKKPPPI 940
 Qy 646 EEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIK-ETKLSAEPAPDFSDYS 704
 ::: |:: ||: : :| | | | : : : | : :
 Db 941 KDSKSLT-----AEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPPNFNTCT 990
 Qy 705 EMAKVE-----QPVPDHSELVE-----DSSPDSEPVDLFSDDS--- 737
 | | :| : | | :| : : :|
 Db 991 ECKNQVCNLCGFNPTPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASMPVPTESSSQK 1050
 Qy 738 --IPDVPQ-----KQD-----ETVML--VKESLTETSFESMIEYENKEKLSALPPEGG 781
 :| || ||: | | :| ||| :| : :| :| :
 Db 1051 TAVP--PQVKLVKKQEVEVKTEAEKVILEKVKETLSMEKI PPMVTTDQKQESKLEKDKA 1108
 Qy 782 KPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPQMEELSTAVYSNDDLFISKEAQIRET 841
 | | | | :| :| : :| | | :| :| :| :
 Db 1109 SALQE--KKPLPEEK-KLIPEE-EKIRSEEKKPLLEKKKPTP---EDKKLLPEAKTSAP 1160
 Qy 842 ETFSD---SSPIEIIIDE-FPTLISSKTDSSFSKLAREYTDLEVSHKSEIANAPDGA-GSLP 896
 | :| :| : :| | | : :| | |
 Db 1161 EEQKHDLLKSQVQIAEEKLEGRVAPKTVQEGK-----QPQTKMEGLPSGTPQSLP 1210
 Qy 897 CTELPHDLSLKNI----QPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQ----- 947
 : | | | || | : :| :| :| :| :| :
 Db 1211 KED---DKTTKTIKEQPQPCTAKPDQEKKEDDKSDTSSSQPKSPQGLSDTGYSSDGISS 1267
 Qy 948 --AEIESIVKPKVLEKEAEKKLPDSTEKEDRSPSAIFSADLGK--TSVVDLL 995
 || |:: ||: | | | : :| | :| | :| :| :|
 Db 1268 SLGEIPSLIPTD--EKDILKGLKKDSFSQESSPS--PSDLAKLESTVLSIL 1315

RESULT 12

PCLO_MOUSE

ID PCLO_MOUSE STANDARD; PRT; 5038 AA.
 AC Q9QYX7; Q9QYX6; Q9QZJ0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Piccolo protein (Presynaptic cytomatrix protein) (Aczonin) (Brain-
 DE derived HLMN protein).
 GN PCLO OR ACZ.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING,
 RP TISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.
 RC TISSUE=Brain;
 RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT900XNczonin, ~~5155W-kdHpnagctive sheiffldiHapgofoeJnfGpresynaptic~~ 66
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 RN [2]
 RP REVISIONS.
 RC TISSUE=Brain;
 RA Kilimann M.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 4502-4682 FROM N.A.
 RC TISSUE=Brain;

 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle
 CC trafficking.
 CC -!- SUBUNIT: Interacts with Rabac1/Pral and profilin.
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
 CC synaptic junctions.
 CC -!- ALTERNATIVE PRODUCTS:
 CC E0ent=Alt06pat1995 splicing; Named ibonding=2alcium and
 CC Name=1;
 CC IsoId=Q9QYX7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9QYX7-2; Sequence=VSP_003928, VSP_003929;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in
 CC stomach. Not detected in other tissues analyzed including adrenal
 CC gland, testis and pancreas.
 CC -!- DOMAIN: C2 domain 1 is
 CC phospholipids. Calcium binds with low affinity but with high
 CC specificity and induces a large conformational change.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----6-----eng-----2;-----
 DR EMBL; Y19185; CAB60731.2; -.
 DR EMBL; Y19186; CAB60732.2; -.
 DR EMBL; AF181269; AAD55786.2; -.

DR HSSP; P04410; 1A25.
 DR MGD; MGI:1349390; Pclo.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0005509; F:calcium ion binding activity; ISS.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . .; ISS.
 DR GO; GO:0005522; F:profilin binding activity; IDA.
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.
 DR GO; GO:0016080; P:synaptic vesicle targeting; NAS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001478; PDZ.
 DR Pfam; PF00168; C2; 2.
 DR Pfam; PF00595; PDZ; 1.
 DR SMART; SM00239; C2; 2.
 DR SMART; SM00228; PDZ; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 DR PROSITE; PS50106; PDZ; 1.
 KW Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;
 KW Repeat; Alternative splicing.
 FT DOMAIN 371 470 10 X 10 AA TANDEM APPROXIMATE REPEATS OF
 FT P-A-K-P-Q-P-Q-Q-P-X.
 FT ZN_FING 502 526 C4-TYPE (POTENTIAL).
 FT ZN_FING 967 990 C4-TYPE (POTENTIAL).
 FT DOMAIN 2305 2329 POLY-PRO.
 FT DOMAIN 4394 4488 PDZ.
 FT DOMAIN 4607 4705 C2 DOMAIN 1.
 FT DOMAIN 4922 5012 C2 DOMAIN 2.
 FT VARSPLIC 4829 4833 TKPTN -> SKRRK (in isoform 2).
 FT /FTId=VSP_003928.
 FT VARSPLIC 4834 5038 Missing (in isoform 2).
 FT /FTId=VSP_003929.
 SQ SEQUENCE 5038 AA; 547600 MW; DADA460CF3B40888 CRC64;

Query Match 5.3%; Score 315; DB 1; Length 5038;
 Best Local Similarity 22.0%; Pred. No. 0.00019;
 Matches 254; Conservative 136; Mismatches 435; Indels 328; Gaps 57;

QY 57 RKPA--AGLSAAPVPTAPAAGAPLMDFG---NDFVPPAP -----GPLPAAPPVAPE 103
 : || || : | | | | : | : | : |
 Db 288 KSPAQPAGTGKSPAQPPTAKPPAQAGLEKTSLQQPGPKSLAQTPGQGVPPGPAKSPA 347
 QY 104 RQ-----PSWDPSP-VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ-A 155
 : | : | | : | | | : | | | | : | | | |
 Db 348 QQPGTAKLPAQQPGPQTASKVPGPTKTPAQLSGPGKTPAQPGPTKPSQQPIPAKPQPQ 407
 QY 156 EPVWT---PPAPAPAAP---STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209
 : || | | || | | || | : : : | | | :
 Db 408 QPVATKPQQPAPAKPQPQHPTPAKPQPQQPTPA-----KPQPQQPTPAKPQP 456
 QY 210 FPSVLLETAASXPSLS-----PLSA--ASFKEHEYLGNLSTVLP---TEGTLQENV 256
 | : : | | | | | | : | : | | |
 Db 457 QHPGLGKPSAQQPSKISQTVTGRPLQAPPTSAAQAPAQGLSKTICPLCNTTELLLTPE 516
 QY 7 EASKEVSEKAKTLI-----DRDLTEFSEL-----EYSEMGSSESVSPPKA 296
 : | : : : : : | | | | : : | : |||
 Db 517 KANFNTCTECQSTVCSLCGFNPNPHLTEIKEWLCLNCQMQRALGGELAAIPSSPQPTPKA 576

Qy 297 ESAVIV-----ANPREEIIVKN---KDEEEK---LVSNNILHX-----QQE 331
 | :|:|:| : | | | | | |
 Db 577 ASVQPATASKSPVPSQQASPKKELPSKQDSPKAPESKKPPPLVKQPTLHGPTPATAPQPP 636

 Qy 332 LPTALTCLV--KEDEVSSSEKAKDSFNEKRVAVEAPMREEYADFKEPFRVWEVKDSKEDS 389
 : || | : :| | | : | : : : ||
 Db 637 VAEALPKPAPPKPSAALPEQAK-----APV---ADVEPKQP--KTTETLTDS 679

 Qy 390 DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYIT 449
 || : | | : | : | : | : | : |
 Db 680 PSSAAATSKPAILSSQVQ---AQAQVTTAPPLKTDSAKTSQSFPPTGD-----T 725

 Qy 450 CAPFN-----PAATESIATNIFPLLEDPTSENXTD-EKKIEEKKAQIVTEKNTSTKTSN 502
 | : || : | : || : : || | | | | | | | K
 Db 726 ITPLDSKAMPRPASDSKIVSH-----PGPTSESKDPVQKKEEPKKAQTKVTPKPDTK--- 777

 Qy 503 PFFVAAQDSETDYVTTDNLTKEVTEE-----VANMPEGLTPDLVQEACE 546
 | : || | : : : : | : | : | |
 Db 778 PVPKGSPTPSGTRPTTGQATPQSQQPPKPPEQSRRFSLNLGGIADAPKS-QPTTPQET-- 834

 Qy 547 SELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLP----DIVM 602
 ||| : : | | : | | | : | | | :
 Db 835 -----VTGKLFGFGASI-FSQASNLIS----TAGQQAPHPQTGPAAPSKQAPPPSQTLLA 884

 Qy 603 EAPLNSA--VPSAGASVIQ-----PSSSPLEASSVNYESI-----KHEP---ENPP 643
 : | | | | | : : ||| : : || | | | |
 Db 885 QGPPKSTGQHPSAPAKTTAVKKETKGPAAENLEAKPAQAPTVKKAEDKKHPPGKVSPP 944

 Qy 644 PYEEAMSVELKVSIGKEEIKEPENINAALQETAPYISACDLIK-ETKLSAEPAPDFSD 702
 | Xs ||| | : : || | : | : : la | : : ter.
 Db 945 P-----TEPEKAVLAQKPKDKTTKPKPACPLCRTELNVGSQDPPNFNT 986

 Qy 703 YSEMAKVE-----QPVPDHSELVE-----DSSPDSEPVD 731
 : | | | : | : | | : | |
 Db 987 CTECKNQVCNLCGFNPTPHLTEIQEWLCLNCQTQRAISGQLGDMDKMPASSGPKASPVP 1046

 Qy 732 LFSD-----DSIPDVPQKQDET-----MLVKESLT 757
 : : : : | : : |
 Db 1047 APAEPPPQKTPTAAHAKGKKKETEVKAETEKQIPEKETPSIEKTPPAVATDQKLESEVT 1106

 Qy 758 ETSFESMIEYENKEKLSAL-----PPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSK 809
 : : : | : | | || | | | | : | | | : | :
 Db 1107 KSLVSVLPEKKPSEEEKALPADKKEKKPPAAEAPPLEEKKPIPDQK--LPPDAKPSASE 1164

 Qy 810 KEKIPLQMEELSTAVYSNDDLFISKEAQIR-ETETFSDV EIIDEFPTLISSKTBKFS 868
 | : : : | : : | | | : | | | : | : | :
 Db 1165 GEE---KRDLLKAHVQIPEEGPIGKVASLACEGEQQPDTRPEDLPGATPQTLPKD----- 1216

 Qy 869 KLAREYTDLEVSHKSEIANAPDGAG--SLPCTELPHDLS--LKNIQPKVEEKISFSDDFS 924
 | : : : | : | | | | | | : | | : | : | :
 Db 1217 ---RQKESRDVTQPQAEGTAKEGRGEPKSDRTEKEEDKSDTSSSQPKSPQGLS-DTGYS 1272

 Qy 925 KNGSATSKVLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA 984
 : | : | || || | : : || : | | : : || : :
 Db 1273 SDGISGS-----LG-----EIPSLIPSD--EKDLLKGLKKDSFSQESSPSS--PS 1313

 Qy 985 DLGK--TSVVDLL 995

Db 1314 DLAKLESTVLSIL 1326

RESULT 13

ANK2_HUMAN

ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunitomo M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [2]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrinB: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q01484-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC Name=3;
CC IsoId=Q01484-3; Sequence=VSP_000268;
CC -!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.

CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -!- SIMILARITY: Contains 23 ANK repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC or send an email to 32Y 00X8 -sib.ch)MID1 094559
CC -----
DR EMBL; X56957; CAA40278.1; -.
DR EMBL; X56958; CAA40279.2; -.
DR EMBL; Z26634; CAB42644.1; -.
DR EMBL; M37123; AAA62828.1; -.
DR PIR; S37431; S37431.
DR HSSP; P42771; 1DC2.
DR Genew; HGNC:493; ANK2.
DR MIM; 106410; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation.
FT REPEAT 63 92 ANK 1.
FT REPEAT 96 125 1200XA K 2. VAPAPAX
FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
FT REPEAT 331 360 ANK 9.
FT REPEAT 364 393 ANK 10.
FT REPEAT 397 426 ANK 11.
FT REPEAT 430 459 ANK 12.
FT REPEAT 463 492 ANK 13.
FT REPEAT 496 525 ANK 14.
FT REPEAT 529 558 ANK 15.
FT REPEAT 562 591 ANK 16.
FT REPEAT 595 624 ANK 17.
FT REPEAT 628 657 ANK 18.
FT REPEAT 661 690 ANK 19.
FT REPEAT 694 723 ANK 20.

Qy	14	DSPP-----RPQPAFKYQFVPEPEDEEEEEEEDEDEDEDEDE-----EVEVDEAK	589860XT
Db	1648	DIPDETQSTQKQHKPSLGIKKPVRRLKEKQKQKEEGLQASAEKAEKKGSSSEESLGED	1707
Qy	59	PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----	92
		: : : :	
Db	1708	P--GLAPEPLPTVKAT-SPLIEETPIGSIKDKVKALQKRVEDEQKGRSKLPIRVKGKEDV	1764
Qy	93	-----PLPAA-PPVAPERQPSWDPSP-----VSSTVPAPSPL	123
		:	
Db	1765	PKKTTHRHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV	1824
Qy	124	SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW	159
		: : : : :	
Db	1825	SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV-	1883
Qy	160	TPPAPAPAAPPSTPAAPKRR--GSSGAVVXXXXKIM	TISAGQEDFPSVLLE 216
		: : : : : :	
Db	1884	SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLPVSPSG	1934
Qy	217	TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT	268
		: : : : : :	

Db 1935 KTEKQPPVSPTSSTERIEETMSVRELMKAFQSGQDPSKHKTGLFEHKSAAKQKQPQEKGV 1994

Qy 269 -----LLIDRDLTEFSELEYSEMGSSFSVSPKAES--AVIVANPREEIIVKNKDE-- 316
:| |: : :| : :| :| :| :| :| :|

Db 1995 RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAEKRGVRVSS----IGVKKEDAAG 2049

Qy 317 -EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV 346
:| :| :| :| :| :| :| :| :| :|

Db 2050 GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGDMDLQISPRKTSTDFSEVI 2107

Qy 347 SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED----- 388
| : | : :| :| :| :| :| :| :|

Db 2108 KQELEDNDKYQQFRLSEETEKALHLDQVLTSPFNTPFLDYMKDEFLPALSLQSGALDG 2167

heobS Qy 389 -SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSESSNDDT FPSTPEGIKDRS 444
| : | : | :| :| :| :| :| :| :|

Db 2168 SSES LNKG VAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT 2225

Qy 445 GAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPF 504
| : :| :| :| :| :| :| :| :| :| :|

Db 2226 G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDESSTESFQKE 2277

Qy 505 FVAAQDSETDYVTTDNLTKVTEEVVA-NMPEGLTPDLVQACESELNEVTGTKIAYETKM 563
:| :| :| :| :| :| :| :| :| :|

Db 2278 ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT---EEAACDEGQRTFGSS-AHKT-- 2330

Qy 564 DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV 610
|| || : :| :| :| :| :| :| :|

Db 2331 ---QTDSEAQES-----TATSDETKALPLPEASVKTDTGTESKPQGVIRSPQGLELAL 2380

Qy XA 1 PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVBG 6582
|| :| :| :| :| :| :| :| :| :|

Db 2381 PSRDSEVL SAVADDS LAVSHKDSLEASPVLEDNSSHKT PDSLEPSPLKESPCRDSLESSP 2440

Qy 658 IKEEIKE---PEN--INAALQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710
: : :| : :| :| :| :| :| :| :| :| :|

Db 2441 VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE 2490

Qy 711 QPVPDHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI 765
| :| :| :| :| :| :| :| :| :|

Db 2491 Q-----TSLMESSGKSPLSPDTPSSEEVSYEVT PKTTDVSTPKPAVIHECAEED----- 2539

Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK---EKIPLQMEELS 821
: || || | | :| :| :| :| :| :| :|

Db 2540 DSENGEKKRFTPEE----T EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEESS 2589

Qy 822 TAVYSNDDLFI SKEA-QIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVS 880
: | :| :| :| :| :| :| :| :| :|

Db 2590 S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSSSES----- 2633

Qy 881 HKSEIANAPDGAGS-----LPCTELPHDL SLKN-----IQPKVEEKISF--SDD 922
: | :| || | :| :| :| :| :| :| :|

Db 2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPLSSMDSNSSPEEVQFQPVVSKQYTFKMNED 2692

Qy 923 FSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSD-----TEKEDRS 977
: : :| :| :| :| :| :| :| :|

Db 2693 TQEEPGKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

RESULT 14

MAPB_HUMAN

ID MAPB_HUMAN STANDARD; PRT; 2468 AA.
AC P46821;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
DE LC1].
GN MAP1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95104835; PubMed=7806212;
RA Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
RT "Cloning of human microtubule-associated protein 1B and the
RT identification of a related gene on chromosome 15.";
RL Genomics 22:273-280(1994).
CC -!- FUNCTION: THE FUNCTION OF BR PS IS ESSENTIALLY UNKNOWN.
CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
CC STABILIZING MICROTUBULES.
CC -!- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
CC WITH MAP1A AND MAP1B PROTEINS.
CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
CC responsible for the binding of MAP1B to microtubules.
CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC from MAP1B by proteolytic processing. It is free to associate with
CC both MAP1A and MAP1B. It interacts with the amino terminal region
CC of MAP1B (By similarity).
CC -!- SIMILARITY: TO MAP1A.
CC -----
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CC -----
DR EMBL; L06237; AAA18904.1; -.
DR Genew; HGNC:6836; MAP1B.
DR MIM; 157129; -.
DR GO; GO:0005875; C:microtubule associaEMBL/omplex; TAS.
DR InterPro; IPR000102; MAP1B_neuraxin.
DR Pfam; PF00414; MAP1B_neuraxin; 10.
DR PROSITE; PS00230; MAP1B_NEURAXIN; 6.
KW Microtubules; Repeat; Phosphorylation.

FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1997 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 5.0%; Score 296.5; DB 1; Length 2468;
 Best Local Similarity 21.5%; Pred. No. 0.00041;
 Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

Qy 2 EDLDQSPLVSSS-DSPPRPQPAFKYQ---FVREP-----EDEE 35
 || :: ||:| || : : | : ::|| | :
 Db 956 EDGEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGAEQ 1015

 Qy 36 EEEEEEEDEDEDLEEELEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPL 94
 ||| :|||: || | | : | | | | | : | | |
 Db 1016 SEEAEDEEDKAEDAREEEYEPEKMEAEYVMAVVDKAAEAGGAEQYGFLLTPTKQLG-- 1073

 Qy 95 PAAPPVAPERQPSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154
 : | | : | | : | | | | : | | | : |
 Db 1074 ---AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120

 Qy 155 AEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----D 209
 : | | | | : | : | | | |
 Db 1121 QSTIEISSEPTPMDEMSTP--- -----RDVMSDETNNETESPSQSESVSVSK 116850XG

 Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259
 : | | | | : : || : | | : | | : | :
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222

 Qy 260 -----KEVSEKAKTLLIDRLTEF-----SELEYSEMGS---SFS 291
 || || | | : | | | : | : | : ||
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPPSKSPSLSPSPSPLEKTPLGERSVNFS 1280

 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328
 ::| ||: | : | : :: : | : | : : |
 Db 1281 LTPNEIKVSAEAEVAPVSPEVTQEVVEEHCASPEDKTLEVVSPSQSVTGSAGHTPYQSP 1340

 Qy 329 ----QQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383
 ||| : : | | : | : : | | | : : |
 Db 1341 TDEKSSHLPTEV--IEKPPAVPVSFEDSDAKDENERASVSPMDEPVPDSESPIEKVLSPL 1398

 Qy 384 DSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDR 443
 | : : : || | : | | | : : | :
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEKSGKQGSPPQVSPVSE----- 1447

 Qy 444 SGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKK-----IEKK-----A 488
 : | | : | : || | || : : : : |

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-142 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=96257242; PubMed=8666295;
 RA Liu D., Fischer I.;
 RT "Isolation and sequencing of the 5' end of the rat microtubule-
 RT associated protein (MAP1B)-encoding cDNA.";
 RL Gene 172:307-308(1996).
 RN [2]
 RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
 RX MEDLINE=92347374; PubMed=1639092;
 RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
 RT "Identification of two distinct microtubule binding domains on
 RT recombinant rat MAP 1B.";
 RL Eur. J. Cell Biol. 57:66-74(1992).
 RN [3]
 RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Spinal cord;
 RX MEDLINE=90059871; PubMed=2555150;
 RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
 RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
 RT "Neuraxin, a novel putative structural protein of the rat central
 RT nervous system that is immunologically related to microtubule-
 RT associated protein 5.";
 RL EMBO J. 8:2879-2888(1989).
 RN [4]
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
 RX MEDLINE=97405699; PubMed=9260743;
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
 RT in rat CNS and PNS during development.";
 RL J. Neurosci. Res. 49:319-332(1997).
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
 CC that accompany neurite extension. Possibly MAP1B Binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
 CC heart or muscle.
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
 CC nerve levels are high early in development but decrease during
 CC postnatal development and are low in adults. In dorsal root
 CC ganglia levels remain high throughout development.
 CC -!- INDUCTION: By nerve growth factor.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated

CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: TO MAP1A.
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to
 CC 2459) was originally described as neuraxin in Ref.3.

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DR EMBL; U52950; AAB17068.1; -.
 DR EMBL; X60370; CAC16162.1; -.
 DR EMBL; X16623; CAA34620.1; ALT_SEQ.
 DR PIR; A56577; A56577.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 8.
 KW Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2459 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1869 1885 MAP1B 1.
 FT REPEAT 1886 1902 MAP1B 2.
 FT REPEAT 1903 1919 MAP1B 3.
 FT REPEAT 1920 1936 MAP1B 4.
 FT REPEAT 1937 1953 MAP1B 5.
 FT REPEAT 1954 1970 MAP1B 6.
 FT REPEAT 1988 2004 MAP1B 7.
 FT REPEAT 2005 2021 MAP1B 8.
 FT REPEAT 2022 2038 MAP1B 9.
 FT REPEAT 2039 2055 MAP1B 10.
 FT DOMAIN 559 1035 GLU-RICH.
 FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 FT DOMAIN 2224 2312 LYS-RICH.
 FT CONFLICT 127 127 M -> V (IN REF. 1).
 FT CONFLICT 140 140 T -> S (IN REF. 1).
 FT CONFLICT 2112 2112 R -> K (IN REF. 3).
 FT CONFLICT 2169 2169 L -> I (IN REF. 3).
 SQ SEQUENCE 2459 AA; 269497 MW; 2E3F6872DEDB8BA2 CRC64;

Query Match 4.9%; Score 289; DB 1; Length 2459;
 Best Local Similarity 20.9%; Pred. No. 0.0008;
 Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

Qy 30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPA 89
 | | ||| |||: :: || :: | | | | : ||:
 Db 1004 EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEDQY--DFL--- 1058
 Qy 90 PRGPLPAAPP--VAPERQPSWDPSVPSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP 147
 || | :| |:| | |:| | | | |:| |
 Db 1059 ---GTPAKQPGVQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF 1106

Qy 148 PASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ 207
|: : | | || : | : | | |
Db 1107 TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNNEETESPSQ 1150

Qy 208 E-----DFPSVLLETAASXP---SLSPLSAASFKE----HEYLGNLSTVLPTEGTLQENV 255
| : | | | : || | : : | : ||: | :
Db 1151 EFPVNTKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF 1210

Qy 256 SEAS-----KEVSEK-----AKTLLIDRDLTE 277
|::: |::|::: || | : | :
Db 1211 SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSPPIEKTPLGERSV-N 1269

Qy 278 FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK----- 314
|| : | : : || | : | | : : : 29NBF 50XS
Db 1270 FSLTPNEIKASAEGEATAVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTPY 1329

Qy 315 ----DEEEKLVSNILHXQQELPTALTCLVKEDEVVSSE--KAKDSFNEKRVAVEAPMRE 368
||: : : | : || | : || | ||: : : || |
Db 1330 QSPTDEKSSHLPTTEVTEAQAQV-----VSFEFTEAKDE-NER--SSISPMDE 1374

Qy 369 EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDDKKCFADSL 415
| : | | : : : || : | | | : || | | : | : |
Db 1375 PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSD-- 1432

Qy 416 EQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNP--AATESIATNIFPLLED- 471
|: | | | : : | : | : | : | : | : |
Db 1433 -----KESPVS-DLTSPLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE 1485

Qy 472 -----PTSENXTDEKKIEEKKAIQVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK 523
|| : : : | : || | : | : | : | : :
Db 1486 RKLGGDGSPTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS 1542

Qy 524 VTEEVVA--NMPEGLTPDLVQACESELNEVTGKIAIYETKMDLVQTSEVMQES-LYPAA 580
|: || : || | | : : | : : : || | ||: : | :
Db 1543 VSTASVATSSFPPTTDD-VSPSLHAEVGSFPHSTEVDDSLSVSVVQTPTTFQETEMSPSK 1601

Qy 581 QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P 611
: || : : : | : : | : | : |
Db 1602 EECPRMSSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHP 1661

Qy 612 SAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG 657
: || : : : | : | : | | : || | : : |
Db 1662 TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEPSYTQDNDLSELISVSQVEASP 1721

Qy 658 IKEEIKEPENINAALQETE-----APYISIACDLIKE---TKLSAEP----- 696
| | : || : | | : : : || :
Db 1722 STSSAHTPSQIASPLQEDTLSDVVPFRDMSLYASLASEKVSLEGEKLSPKSDISPLTPR 1781

Qy 697 -----APDFSDYSEMAK-----VEQPVPDHSELVEDS----- 723
: | || : || : | | : : | :
Db 1782 ESSPTYSPGFSDSTSGAKESTAAYQTSSSPPIDAAAAEPYGRSSMLFDTMQHHLALSRL 1841

Qy 724 -----SPDSEPVDLFSDD---SIPDVP---QKQD 746
|| | | | : || : :
Db 1842 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYGYEYKTE 1901

Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797

Db	1902	RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTRTPEEGGYSY-----EISEK	1953
Qy	798	TLLPDEV--TLKKKEKIPLQMEELSTAVYSNDD-----LFISKEA	836
Db	1954	TTRTPEVSGYTYEKTERRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES	2013
Qy	837	QIRETETFSDDSP-----IEIIDEFPTLISSKTDSFSKLAREYT-----DL	877
Db	2014	YSYETTTKTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL	2073
Qy	878	-----EVSH-KSEIANA---PDG---AGSLPCTELPHDLSLKNIQP-----KV	913
Db	2074	CLVSSCEFKHPKTELSPSFINPNLEWFAGEEPTESERPLTQSGGAPPPSGGKQGRQC	2133
Qy	914	EEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKK-LPSD--	970
Db	2134	DETPPTSVSESAPSQTDSDV---PPETE-----ECPSITADANLDSEDESETIPTDKT	2183
Qy	971	-----TEKEDRSPS-----AIFSADLGKTSVVDLLYWRDIKKTG	1004
Db	2184	VTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAEQNLGKALKKDLKEKAKTKKPG	2240

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Job time : 25.6482 secs